Н

```
RESULT 2
US-10-232-188-5
; Sequence 5, Application US/10232188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 13345, A
Sequence 13346, A
Sequence 1, Appli
Sequence 4, Appli
Sequence 322, Appli
Sequence 352, Appli
Sequence 352, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332, App
13113, A
5, Appli
13128, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2, Appli
13111, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13350,
13336,
                                                                 December 16, 2005, 16:38:19; Search time 107.547 Seconds (without alignments) 590.532 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13355,
                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                       1 MANLERTFIAIKPDGVQRGL........WFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3
Sequence 3
Sequence 4
Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Sequence Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                               Published Applications AA Main: *
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: *
3: /cgn2_6/ptodata/1/pubpaa/US10A-PUBCOMB.pep: *
4: /cgn2_6/ptodata/1/pubpaa/US10A-PUBCOMB.pep: *
5: /cgn2_6/ptodata/1/pubpaa/US10B-PUBCOMB.pep: *
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep: *
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-232-188-5

US-10-133-628-12

US-10-133-628-12

US-10-732-923-13345

US-10-732-923-13346

US-10-732-923-13346

US-10-732-923-13127

US-10-732-923-13127

US-10-732-923-1313

US-10-732-923-1313

US-10-732-923-13119

US-10-732-923-13119

US-10-732-923-13356

US-10-732-923-13356

US-10-732-923-13356

US-10-732-923-13356

US-10-732-923-13336

US-10-732-923-13336

US-10-732-923-13336

US-10-732-923-13336

US-10-732-923-13336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-791-118A-2
US-10-732-923-13111
US-10-732-923-13110
                                                                                                                                                                                                                        of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-791-118A-3
                                                                                                                                                                                                1867569 segs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             protein search, using sw model
                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                US-10-074-694-5
803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          %
Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0
100.0
100.0
99.4
99.4
99.4
99.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.9
93.5
93.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                             Perfect score:
                                                ı
                                                                                                                                                                                                                          Total number
                                              OM protein
                                                                                                                                                                                                   Searched:
                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
```

```
y character introversations:

APPLICANT: Werner, Sabine
APPLICANT: Werner, Sabine
APPLICANT: Braub, Susanne
APPLICANT: Penzberg, Jorn-Peter
APPLICANT: Penzberg, Jorn-Peter
APPLICANT: Penzberg, Jorn-Peter
APPLICANT: Regenbogen, Johannes
TITLE OF INVENTION: Use of polypeptides or nucleic acids
TITLE OF INVENTION: encoding these of the gene family NM23 for the diagnosis or
TITLE OF INVENTION: treatment of skin or intestinal disorders, and their use for TITLE OF INVENTION: the identification of pharmacologically
TITLE OF INVENTION: the identification of pharmacologically
TITLE OF INVENTION: the identification of pharmacologically
TITLE OF INVENTION: active substances
TITLE OF INVENTION: active substances
TITLE OF INVENTION: do not see the see the see the see that the second of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                       426, App
13340, A
2, Appli
42, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                            13320, A
21, Appl
2, Appli
13132, A
                     Appli
Appli
, Appl
                                                                                           13341, A
13112, A
19, Appl
19, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                    Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                     Sequence
   Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
US-10-732-923-13354
US-09-791-118A-1
US-10-232-188-4
US-10-33-628-11
US-10-732-923-13341
US-10-732-923-13341
US-10-732-923-13341
US-10-732-923-13340
US-10-732-923-13340
US-10-732-923-13340
US-10-732-923-13340
US-10-733-923-13320
US-11-033-628-2
US-10-733-923-13320
US-10-733-923-13320
US-10-733-923-13320
US-10-733-923-13320
US-10-733-923-13320
US-10-733-923-13320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 803; DB 3;
100.0%; Pred. No. 1.5e-82;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09791118A Patent No. US20020034741A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 152; Conservative
     1152
1152
1152
1152
1152
1177
1177
1178
1180
1180
1180
1152
1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
     JS-09-791-118A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-791-118A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 3
LENGTH: 152
```

ö

Gaps

ö

Length 152; 0; Indels

```
1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                    100.0%; Score 803; DB 4;
100.0%; Pred. No. 1.5e-82;
iive 0; Mismatches 0;
                   CURRENT APPLICATION NUMBER: US/10/133,628 CURRENT FILING DATE: 2002-04-29 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 90, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION;
APPLICANT: DEPRIMO, SAMUEL
FILE REFERENCE: 03495.0227-00000
                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 152, Conservative
                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 152; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-10-440-464-90
                                                                                                                                                                                                           US-10-133-628-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-440-464-90
                                                                                                               SEQ ID NO 12
LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 유
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASBEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GALLOIS-MONTBRUN, SARAH
APPLICANT: GALWEIDER, BENOIT
APPLICANT: GIACOMOLI-EERNANDES, VERONIQUE
APPLICANT: DEVILLE-BONNE, DOMINIQUE
APPLICANT: VERON, MICHEL
TITLE OF INVENTION: MICHEL
TITLE OF INVENTION: ANTIVATION AND THERAPEUTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 803; DB 4; Length 152; Best Local Similarity 100.0%; Pred. No. 1.5e-82; Matches 152; Conservative 0; Mismatches 0; Indels
                   GENERAL INFORMATION:
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 28-Aug-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/713,825
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Bllings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0124 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastERQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/232,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELBERONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 12, Application US/10133628
; Publication No. US20030207830A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
Publication No. US20030022306A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: GenBank
                                                                                                                                                                                                                                                            COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: 127983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE
                                                                                                                                                                                                                                 STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-133-628-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-232-188-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

```
APPLICANT: O'FARRELL, ANNE-MARIE
APPLICANT: O'FARRELL, ANNE-MARIE
APPLICANT: SMOLICH, BEVERLY
APPLICANT: MANNING, WILLIAM
APPLICANT: MANNING, WILLIAM
APPLICANT: MANNING, WILLIAM
APPLICANT: MANTER, SARAH
APPLICANT: CHERRINGTON, JULIE
APPLICANT: AND ACTIVITY IN MAMMALS
TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
FILE REFERENCE: 036602/1592
CURRENT PILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: 60/448,922
PRIOR APPLICATION NUMBER: 60/448,922
PRIOR APPLICATION NUMBER: 60/448,874
PRIOR FILING DATE: 2003-02-24
PRIOR FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 185
SOFTWARE: PATCHILING DATE: 20.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                           61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                        61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
         09
1 MANLERTFIAIKPDGVQRGLVGBIIKRFEQKGFRLVAMKFLRASEBHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQXGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cch 100.0%; Score 803; DB 4; al Similarity 100.0%; Pred. No. 1.5e-82; 152; Conservative 0; Mismatches 0;
                                                                                                                                                                                                    121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                        121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
```

```
Sequence 1, Application US/11013684

Publication No. US2005013648941

GENERAL INFORMATION:
TITLE OF INVENTION:
PILE REFERENCE: 04P0019

CURRENT FILING DATE: 2004-12-17

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKRGTIRGDFCIQVGRNIIHGSD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Human NDPK-B: N115S OTHER INFORMATION: protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 PGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SCHNEIDER, BENOIT
APPLICANT: GIACOMONI-PERNANDES, VERONIQUE
APPLICANT: GIACOMONI-PERNANDES, VERONIQUE
APPLICANT: DEVILLE-BONNE, DOMINIQUE
APPLICANT: DEVILLE-BONNE, DOMINIQUE
APPLICANT: VERON, MICHEL
TITLE OF INVENTION: MUTANT NDP KINASES FOR ANTIVIRAL NUCLEOTIDE ANALOG
FILLE REFERENCE: 03495.0227-00000
CURRENT APPLICATION NUMBER: 105/10/133,628
CURRENT FILING DATE: 2002-04-29
NUMBER OF SEQ ID NOS: 27
SOFTWARDER: COMPANDED TO THE TOTAL NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        query Match 99.4%; Score 798; DB 4; Length 152;
Best Local Similarity 99.3%; Pred. No. 5.4e-82;
Matches 151; Conservative 1; Mismatches no تعمام
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
99.4%; Score 798; DB 6; 1
Best Local Similarity 100.0%; Pred. No. 5.3e-82;
Matches 151; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 SVKSAEKEISLWPKPEELVDYKSCAHDWVYE 151
121 SVKSAEKEISLWFKPEELVDYKSCAHDWVYE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10133628; Publication No. US20030207830A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-133-628-4
                                                                                             US-11-013-684-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-10-133-628-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-013-684-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122
                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ଚ
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKFGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MANLERIFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; gequence 13346, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT PELICAN NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13346
                                                                                                                                   Sequence 13345, Application US/10732923

Publication No. US20050108791A1

GENERAL INFORMATION:

APPLICANT Edgerton, Michael D

TITLE OF INVENTION:

FILE REFERENCE: 38-15(52796)C

CURRENT APPLICATION UNMER: US/10/732,923

CURRENT PILING DATE: 2003-12-10

PRIOR PILING DATE: 2003-12-04

NUMBER OF SEQ ID NOS: 24149

SEQ ID NO 13345

LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 803; DB 5; Length 152; Best Local Similarity 100.0%; Pred. No. 1.5e-82; Matches 152; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.4%; Score 798; DB 5; I
100.0%; Pred. No. 5.3e-82;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                         DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-732-923-13345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-732-923-13346
                                                                                                                         US-10-732-923-13345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-10-732-923-13346
                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
```

ò

ઠ

ö

유

ઠે

ö

```
US-09-791-118A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-791-118A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JAPPLICANT: Jackson, Stuart E.; Lincoln, Stephen B.;
APPLICANT: Jackson, Stuart E.; Lincoln, Stephen B.;
APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
APPLICANT: Chalup, Mischael S.; Jackson, Jennifer L.;
APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
APPLICANT: Gerstin, Jr., Panzer, Scott R.;
APPLICANT: Gratin, Jr., Panzer, Scott R.;
APPLICANT: Plores, Vincent Z.; Daffo, Abel;
APPLICANT: Chang, Simon C.; Au, Alian P.;
APPLICANT: Chang, Simon C.; Au, Alian P.;
APPLICANT: Chang, Stebekah R.
TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT FILE REFERENCE: PT-1183 US/
CURRENT APPLICATION NUMBER: US/10/363,829
CURRENT FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: US 60/229,751
PRIOR APPLICATION NUMBER: US 60/229,751
PRIOR APPLICATION NUMBER: US 60/229,751
PRIOR APPLICATION NUMBER: US 60/229,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
FRIOR APPLICATION NUMBER: 10/310,154
FRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 98.9%; Score 794; DB 5; Length 152; Best Local Similarity 98.0%; Pred. No. 1.5e-81; Matches 149; Conservative 2; Mismatches 1; Indels
                                                                                                                121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSVESAEKEIGLWFKPEELIDYKSCAHDWVYE 152
                                                                                       DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                        Sequence 13127, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 352, Application US/10363829; Publication No. US20040142331A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-732-923-13127
                                                                                                                                                                                                                                                    US-10-732-923-13127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 13127
                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
APPLICANT: Branch Sugarine Peter
APPLICANT: Penzberg, Jorn-Peter
APPLICANT: Regenbogen, Johannes
APPLICANT: Regenbogen, Johannes
TITLE OF INVENTION: Use of polypeptides or nucleic acids
TITLE OF INVENTION: Leatment of skin or intestinal disorders, and their use for TITLE OF INVENTION: the identification of pharmacologically
TITLE OF INVENTION: active substances
TITLE OF INVENTION: 000-02-22
CURRENT APPLICATION NUMBER: US/09/791,118A
CURRENT PILING DATE: 2000-04-24
PRIOR FILING DATE: 2000-04-24
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FREUSE FREUSE: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCLQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
PRIOR FILING DATE: 2000-09-05
PRIOR PLING DATE: 2000-09-05
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-05
PRIOR PLING DATE: 2000-09-05
PRIOR PLING DATE: 2000-09-05
PRIOR PLING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-05
PRIOR PLING DATE: 2000-09-06
PRIOR PRIOR PRIOR APPLICATION NUMBER: US 60/230,597
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PRIOR PRIOR APPLICATION DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PRIOR DATE: 2000-09-06
PRIOR APPLICATION NUMBER: US 60/230,597
PRIOR PLING DATE: 2000-09-06
PRIOR DATE: 2000-09-09
PRIOR DATE: 2000-09-09
PRIOR DATE: 2000-09-09
PRIOR DATE: 2000-09-09
P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 MANLERTFIAIKPDGVQRGLVGBIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MANLERIFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASBEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature; OTHER INFORMATION: Incyte ID No: LG:1098570.1.orf3:2000SEP08
US-10-363-829-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.9%; Score 794; DB 4; Length 190; 98.0%; Pred. No. 2e-81; .ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 DSVESAEKEIGLWFKPEELIDYKSCAHDWVYE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09791118A; Patent No. US20020034741A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.0°
Matches 149, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Werner, Sabine APPLICANT: Braun, Susanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
```

g

g 8 셤 ò

```
ö
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                    61 FPGLVKXMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FPGLVKYMNSGPVVAMVWEGLAVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                              1 MANLERIFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRSIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDHKDRPF
                                                                                                                                                                                                                                                                              1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GALLOIS-MONTBRUN, SARAH
APPLICANT: GALLOIS-MONTBRUN, SARAH
APPLICANT: SCHNEIDER, BENOIT
APPLICANT: GALCOMONI-FERNANDES, VERONIQUE
APPLICANT: DEVILLE-BONNE, DOMINIQUE
APPLICANT: DEVILLE-BONNE, DOMINIQUE
APPLICANT: DEVILLE-BONNE, DOMINIQUE
APPLICANT: DEVILLE-BONNE, DOMINIQUE
TITLE OF INVENTION: MICHEL
TITLE OF INVENTION: MCTATION AND THERAPEUTIC USES THEREOF
FILE REFERENCE: 03495, 0227-00000
CURRENT APPLICATION NUMBER: US/10/133,628
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 5
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Human NDPK-B: OTHER INFORMATION: L55H-N115S protein sequence US-10-133-628-5
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13128, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgetton, Michael D
; TITLE OF INVENTION:
; FILE REFERENCE: 38-15(52796)C
                                                                                                                                          Query Match

98.8%; Score 793; DB 5; Length 152;
Best Local Similarity 98.0%; Pred. No. 2e-81;
Matches 149; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.5%; Score 791; DB 4; Length 152; 98.7%; Pred. No. 3.3e-81; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DSVESABKEIHLWFKPEELIDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 5, Application US/10133628
; Publication No. US20030207830A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 150; Conservative
                          TYPE: PRT
CORGANISM: Mus musculus
US-10-732-923-13113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-10-732-923-13128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 152
LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Severate of the several severa
                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                              61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                              61 PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                           1 MANLERIFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MANLERIFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                       1 MANLERIFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 793; DB 3; Length 152;
Pred. No. 2e-81;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.8%; Score 793; DB 4; Length 152; 98.0%; Pred. No. 2e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                               121 DSVESAEKEIHLWFKPEELIDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                       ecn 98.8%; al Similarity 98.0%; 149; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.0°
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-10-732-923-13113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-116-275-332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-116-275-332
                                Query Match
Best Local S
Matches 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
```

а

g

ò

ઠે

```
0; Gaps
                                                                                                                                                Query Match 98.0%; Score 787; DB 5; Length 152; Best Local Similarity 97.4%; Pred. No. 9.5e-81; Matches 148; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                         ; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13128
; LEWOTH: 152
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-732-923-13128
                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                   S d
                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                     ઠે
```

Search completed: December 16, 2005, 17:01:37 Job time : 108.547 secs

ö

```
Sequence 1577, Applequence 96, Applequence 96, Applequence 9110, Applequence 4110, Applequence 4110, Applequence 4110, Applequence 600, Applequence 297, Applequence 3124, Applequence 412, Applequence 412, Applequence 412, Applequence 412, Applequence 412, Applequence 42, Applequence 43, Applequence 256, Applequence 266, Applequence 47, Applequence 47, Applequence 276, Applequence 2768, Appleq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2758, Ap
Sequence 6728, Ap
Sequence 31, Appl
                                                                                                                                  December 16, 2005, 16:39:14 ; Search time 6.69182 Seconds (without alignments) 153.021 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                       1 MANLERTFIAIKPDGVQRGL.....WFKPBELVDYKSCAHDWVYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata///pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata///pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata///pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata///pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata///pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata///pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata///pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata///pubpaa/US11_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-821-234-1577
US-10-878-556A-49
US-11-055-822-966
US-11-055-822-9966
US-10-763-712A-118
US-10-763-712A-118
US-10-793-62-3294
US-10-793-62-3294
US-10-793-62-3294
US-10-793-62-3294
US-10-793-62-326
US-11-074-176-96
US-11-074-176-96
US-11-074-176-96
US-11-074-176-96
US-11-074-176-96
US-11-074-176-96
US-11-074-176-96
US-11-074-176-96
                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA New:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                      51470 seqs, 6736768 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                 US-10-074-694-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152
1352
1356
1356
1357
1357
1152
1152
1162
1163
1163
1163
1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335.5
335.5
307
78
                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                          OM protein
                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                         <u>Б</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1577, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Andarmani, Susan

FILE REFRENCE: 821A

CURRENT PLILNG DATE: 2004-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: PL SEQ_Genes Version 1.0

SEQ ID NO 1577

LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                 3, Appli
60, Appli
60, Appli
7548, Ap
7548, Ap
1658, Ap
1658, Ap
1658, Ap
1184, Ap
1182, Ap
1182, Ap
1182, Ap
1182, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 803; DB 6; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.1e-78;
Matches 152; Conservative 0; Mismatches 0; Indels
                                        US-110-467-657-4834
US-110-485-517-316
US-111-053-076-190
US/11/062
US/11/062
US-11-074-176-240
US-11-062
US-11-090-439-42
US-110-391-626-26
US-110-391-626-26
US-110-391-626-318
US-110-467-657-1654
US-110-467-657-1654
US-110-467-657-1654
US-110-467-657-1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
    349
428
3933
1100
1067
1302
244
244
346
346
347
1104
1104
1104
206
696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CORGANISM: Homo sapiens
US-10-821-234-1577
  US-10-821-234-1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-10-878-556A-49
  121
```

Sequence 49, Application US/10878556A
Publication No. US20050266399A1
GENERAL INFORMATION:
APPLICANT: HOFfmann La-Roche Inc.
TITLE OF INVENTION: HCV regulated protein expression
FILE REFERENCE: 21762

DB 7;

```
66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          :|||:|||:||
123 ESAEREISIWF 133
                                                                                                                                                                                                                                                                                                                                                                        124 KSAEKEISLWF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
   Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-11-055-822-994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-055-822-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFWQASEDLLKEHYVDLKDRPF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pompejus, Markus
APPLICANT: Rroger, Burkhard
APPLICANT: Schroder, Harrwig
APPLICANT: Schroder, Harrwig
APPLICANT: Schroder, Harrwig
APPLICANT: Schroder, Harrwig
APPLICANT: Glader, Oskar
APPLICANT: Laberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: ORNABER: US/11/055,822
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT PILING DATE: 2005-05-01
PRIOR APPLICATION NUMBER: 00/140,031
PRIOR FILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-03
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                    89.7%; Score 720; DB 6; Length 152;
88.2%; Pred. No. 7.5e-70;
tive 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 152
                                                                                                                                                                                                                 ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATRASE ACCESSION NUMBER: sw hum/ndka_human
DATRABASE ENTRY DATE: 1990-04-01
CURRENT APPLICATION NUMBER: US/10/878,556A CURRENT FILING DATE: 2004-06-28 NUMBER OF SEQ ID NOS: 199 SOFTWARE: Patentin version 3.1 SEQ ID NO 49 LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 966, Application US/11055822
Publication No. US20050260707A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.2%
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                           US-10-878-556A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -11-055-822-966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 966
                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
65 VKYMNSGPVVAMVWEGLNVVKTGRVMLGETNP-ADSKPGTIRGDFCIQVGRNIIHGSDSV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 VKYMNSGPVVAMVWEGLNVVKTGRVMLGETNP-ADSKPGTIRGDFCIQVGRNIIHGSDSV 123
                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ERTLILIKPDGVTNGHVGEIIARIERKGLKLAALDLRVADRETAEKHYEEHADKPFFGEL
                                                                                                                                                                                                                  3 ERTLILIKPDGVTNGHVGEIIARIERKGLKLAALDLRVADRETAEKHYEEHADKPFFGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 ERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFFPGL
                                                                                                                                                                    ERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASBEHLKQHYIDLKDRPFFPGL
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Pompejus, Markus

APPLICANT: Rocager, Burkhard

APPLICANT: Schroder, Hartwig

APPLICANT: Schroder, Hartwig

APPLICANT: Zelder, Oskar

TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING

TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS

TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS

FILE REFERENCE: BGI-1210PCN

CURRENT FILING DATE: 2000-06-23

CURRENT FILING DATE: 2000-06-23

PRIOR FILING DATE: 1999-06-25

PRIOR FILING DATE: 1999-06-25

PRIOR PLICATION NUMBER: 60/141,031

PRIOR PLICATION NUMBER: 60/148,613

PRIOR PLICATION NUMBER: 60/148,613

PRIOR PLICATION NUMBER: 60/148,613

PRIOR PLICATION NUMBER: DE 19931415.2

PRIOR PLICATION NUMBER: DE 19931418.7

PRIOR PLILING DATE: 1999-07-08

PRIOR PLING DATE: 1999-07-08

PRIOR PRIOR PRIOR PRIOR DATE: 1999-07-08
                                                                                        ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.8%; Score 335.5; DB 7; Length 136; 50.4%; Pred. No. 4.8e-29; tive 23; Mismatches 41; Indels 1
Length 136;
                                                                                    41; Indels
    41.8%; Score 335.5; DB 7
50.4%; Pred. No. 4.8e-29;
                                 50.4%; Prec. .v.
tive 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 994, Application US/11055822
Publication No. US20050260707A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 KSAEKEISLWF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

7;

----FANNLAQAL 312

```
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: CANCERS
FILE REFERENCE: AM101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT APPLICATION NUMBER: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/10525710
Publication No. US20050260721A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zelder, Oskar
APPLICANT: Schooler, Hartwig
APPLICANT: Schooler, Hartwig
APPLICANT: Hafner, Stefan
APPLICANT: Sulphouge, Containing
TITLE OF INVENTION: Bulphur (metY)
FILE REFERENCE: 13111-00006-US
FILE REFERENCE: 13111-00006-US
CURRENT FILING DATE: 2005-02-24
PRIOR APPLICATION NUMBER: PCT/EP 2003/009453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        504 VVGSNMDKIYIVMNYVEHDLKSLMBTMKQPPLPGEVKTL----MIQLLRGVKHLHDNWIL 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 LNVVKTGRVMLGETNPADSKPGTIR-GDFCIQVGRNIIHGSDSVKSAEKEISLWFKPEEL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444 IEEGTYGVVYRAKDKKTDEIVALKRLKMEKEKEGFPITSLREINTILKAQHPNIVTVREI 503
                                                                                62 PGLV-KYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFC1QVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 -----HLKQHYI--DLKD-----RPFFPGLVKYMNSGPVVAMV------WEG
                                             7 TPIAIKPDGVQRGLVGEIIK-----RFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50; Indels
58; Indels
                                                                                                                                                                             16 VQRGLVGEIIKRFEQKGFRLVAMKFLRASEE-----
                                                                                                                                                                                                                                                                                  313 ELVYFIERAIDLLDEALAKWPIKPRDEVEIK 343
                                                                                                                                                                                                                                                        121 DSVKSAEKEISL-----W-FKPEELVDYK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
8.7%; Score 69.5; DE
Best Local Similarity 18.6%; Pred. No. 8.4;
Matches 36; Conservative 33; Mismatches
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49, Application US/10770726
Publication No. US20050266409A1
GENERAL INFORMATION:
APPLICANT: Wyeth
25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 V----DYKSCAHDW 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        609 LLGAKEYSTAVDMW 622
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             US-10-770-726-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-770-726-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 49
Matches
                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ### APPLICANT: Dillon, Harrison F.
TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
TITLE OF INVENTION: Production
FILLE REFERENCE: H2042101-CIP
CURRENT APPLICATION NUMBER: US/10/763,712A
CURRENT APPLICATION NUMBER: US 10/287,750
FRIOR APPLICATION NUMBER: US 10/287,750
FRIOR APPLICATION NUMBER: US 10/281,010
FRIOR PILING DATE: 2003-01-04
FRIOR PILING DATE: 2003-04-12
FRIOR PELING DATE: 2003-04-12
FRIOR FILING DATE: 2003-09-03
NUMBER OF SEQ ID NOS: 184
SOFTWARE: Patentin version 3.2
SEQ ID NO 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 LVEFWIGGPVMIQVLEGENAVLKNRELMGATNPTEAAEGTIRADFATSVSINAVHGSDSV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 LVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFC1QVGRNIIHGSDSV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 LERTFIAIKPDGVORGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKOHYIDLKDRPFFPG
                                                                                                                                                                                                                                                                        APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Blisabetta
TITLE OF LINENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 4110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 38.2%; Score 307; DB 6; Length 141; Best Local Similarity 43.4%; Pred. No. 5.3e-26; Matches 59; Conservative 27; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.7%; Score 78; DB 6; Length 428; 22.5%; Pred. No. 0.48;
                                                                                                  RESULT 5
US-10-467-657-4110
; Sequence 4110, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 118, Application US/10763712A Publication No. US20050266541A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 KSAEKEISLWFKPEEL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::| ||: :|
ENAALEIAYFFSQTEI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT; ORGANISM: Pyrococcus furiosus
US-10-763-712A-118
                                                                                                                                                                                                                                APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
:[||:||:||
ESAEREISIWF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Solazyme, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-467-657-4110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-763-712A-118
```

ò g ઠે 셤

ઠે

9

Gaps

75;

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                               64 LVKYMNSGPVVAMVWEGLNVVKTGRVMLGE-----TNPADSK------100
                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| :: |: | :| | :| | SLGKSYDAVFPLLHGPNGEDGTIQGLFEVLDIPYVGNGVLAASSSMDKLVMKQLFEHRGL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 PQLPYISFLRSEYEKYENNIIKLVNDKLTYPVFVKPANLGSSVGISKCNNEEELKSGIAE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 NLERIFIAIKP-----DGVQRGL-----VGE-----IIKR-FEQKGF 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3294, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PUBJ48002
CURRENT APPLICATION NUMBER: US/10/793,626
PRIOR PILING DATE: 2004-03-04
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3294
                                                                                                                                                                                                                                                                                                                                      21 VGEIIKRFEQ----KGFRLVAMKFLRASE-----EHLKQH-----YIDLKDRPFFPG
                                                                                                                                                                                                                                                                                           53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.4%; Score 67.5; DB 6; Length 371;
21.9%; Pred. No. 5.2;
tive 25; Mismatches 45; Indels 55
                                                                                                                                                                                                                                             Query Match 8.5%; Score 68.5; DB 6; Length 430; Best Local Similarity 22.4%; Pred. No. 4.9; Matches 33; Conservative 15; Mismatches 46; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 -RLVAMKFLRASEEHLKQHYIDL-KDRPFFPGLVKYMNSGPVVA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------MVWEGLNVVKTGRVMLGETNPADSKPGTIRGD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 AFQFDRKLVIEQGINAREIEVAVLGNDYPETTWPGEVVKD 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 -----PGTIRGDFCIQVGRNIH 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 AEQRDAGVTPGMIR----LSVGTESIH 415
                           102 39 082.7
PRIOR FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: DE 102
PRIOR FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.3
SEQ ID NO 8
LENGTH: 430
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                               ; ORGANISM: Bacillus halodurans
US-10-525-710-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 35; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-10-793-626-3294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-793-626-3294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

; Sequence 600, Application US/10995561 ; Publication No. US20050272054A1 L; GENERAL INFORMATION:

US-10-995-561-600

```
APPLICANT: Trepod, Catherine
APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND METF
TITLE OF INVENTION: USE
FILE REFERENCE: 00592.US1 (MER 268.05920101)
CURRENT APPLICATION NUMBER: US/11/194,246
CURRENT APPLICATION NUMBER: US/11/194,246
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ų,
                                                     CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 KFL-----RASEEHLKQHYIDLKDRPFPPG------LVKYMNSGPVVAMVWE-- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2666, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY. WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 PDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFFPGLVKYMNSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34; Indels
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASESO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 -----GLNVVKTGRVMLGETNPADSKPGTIRGDFCIQV 112
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
8.2%; Score 66; DB 7;
Best Local Similarity 22.5%; Pred. No. 2.1;
Matches 23; Conservative 17; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                               8.4%; Score 67.5; D
23.5%; Pred. No. 52;
Live 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : ::|: | : |:: | | 367 LSRIIWKALKPLLVGKILYTPDTPA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 VVAMVWEGLNVVKTGRVMLGETNPA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 297, Application US/11194246; Publication No. US20050272089A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: HAEMOPHILUS INFLUENZAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Conservative
                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-10-793-626-2666
                                                                                                                                                                                                                                                                                                                                                               US-10-995-561-600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-11-194-246-297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-11-194-246-297
                                                                                                                                                                                                                                                     SEQ ID NO 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
```

```
US-10-793-626-412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-055-822-308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 308
LENGTH: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 PEHRGLPQLPYISFLRSEYEKYENNIIKLVNDKLTYPVFVKPANLGSSVGISKCNNEEEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 FIAIKPDGVQRGLVGEIIKRFEQK-----GFRLVAMKFLRAS--EEHLKQHYIDLKDR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 PFFPGLVKYMNSGPVVAMVWEGLNVVKT-GRVMLGETNPADS----KPGTIRGDFCIQV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Publication No. US2005025478A1

Publication No. US2005025478A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KINMERLY, WILLIAM JOHN
APPLICANT: KINMERLY, WILLIAM JOHN
TITLE OF INVERTION: STARHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3314
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.2%; Score 65.5; DB 6; Length 459;
Best Local Similarity 26.9%; Pred. No. 11;
Matches 32; Conservative 16; Mismatches 54; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: synthetic // OTHER INFORMATION: amino acid sequence US-10-793-626-3314
                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; ; OTHER INFORMATION: amino acid sequence
US-10-793-626-2666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Mismatches 39; Indels 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 FEOKGF-RLVAMKFLRASEEHLKQHYIDL-KDRPFFPGLVKYMNSGPVVA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----MVWEGLNVVKTGRVMLGETNPADSKPGTIRGD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 KSGIAEAFQFDRKLVIEQGINAREIEVAVLGNDYPETTWPGEVVKD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

8.1%; Score 65; DB 6; Length 230;
Best Local Similarity 23.6%; Pred. No. 5.2;
Matches 25; Conservative 16; Mismatches 39; Indels
               CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 2666
LENGTH: 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 308, Application US/11055822 Publication No. US20050260707A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
FILE REFERENCE: PU3480US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-793-626-3314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-055-822-308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94
                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
```

```
143 -----HRLNINLLGEAVLGRKEAAKHLDDTVR----LLRRPDVEYVSIKVSSVASQISMW 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 412, Application US/10793626
Publication No. US2005025547841
GENERAL INFORMATION:
TATLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TILE REPERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR PILING DATE: 1999-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 VAMYWEGLNYVYTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVKSAEKEISLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 VORG-LVGEIIKRFEQKGFRLVAMKFLRASEEHLKOHYI-DLKDRPFFPGLVKYMNSGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - See File Wrapper or PALM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.1%; Score 65; DB 7; Length 1152; 24.6%; Pred. No. 41; Live 21; Mismatches 53; Indels
                                                                                                                   TITLE OF INVENTION: METABOLLC FAIRWAY FROID
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILMG DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR PELICATION NUMBER: 00/141,031
PRIOR PELICATION NUMBER: 60/141,031
PRIOR PELICATION NUMBER: 60/142,101
PRIOR PELICATION NUMBER: 60/148,613
PRIOR PLILNG DATE: 1999-06-25
PRIOR PLILNG DATE: 1999-06-25
PRIOR PLILNG DATE: 1999-06-12
PRIOR PLILNG DATE: 1999-06-12
PRIOR PELING DATE: 1999-06-10
PRIOR PELING DATE: 1999-07-01
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
PRIOR PLING DATE: 1999-07-08
PRIOR PELING DATE: 1999-07-08
PRIOR DATE: 1999-07-08
PRIOR DATE: 1990-07-08
PRIOR DATE: 1990-07-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 412
LENGTH: 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 -FKPEELVDY 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | |: |:|
194 GF--EDTVNY 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
```

US-10-793-626-412

Search completed: December 16, 2005, 17:01:58 Job time: 7.69182 secs

```
Protein o
Human NM2
Human PKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human pro
Human pro
Nucleotid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human nm2
Human nm2
Mature hu
Novel hum
Human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antipsori
Human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NM2
Human NM2
Human nm2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO polyp
Novel bro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour-as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lung smal
                                                                                                                                              December 16, 2005, 16:31:59; Search time 138.333 Seconds (without alignments) 527.255 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                    1 QSQPAVKPCHLKGTMANSER..........WFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aae21724 | Adr66938 | Adr66040 | Abb99909 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aav62505 1
Aag79338 1
Adf76437 1
Ad182817 1
Adn05777 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adp54261 1 Adp23235 Adp2448 Adw06448 Adw08712 Ad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aea90110 | Aeb87772 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aab14823 | Aao26422 | Aag79335 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aau69421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2443163
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                   2443163 segs, 439378781 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP23235
ADU06448
ADW08712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADR66040
ABB99909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADN05777
ADO19200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB14823
AAO26422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR11903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABM81903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADR66938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADF76437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL82817
                                                                                                                                                                                                                                                                                                                                                                                 Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     geneseqp1980s:*
geneseqp1990s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            geneseqp2000s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        geneseqp2004s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  geneseqp2005s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length DB
                                                                                                                                                                                                                                                       US-10-074-694-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_Geneseq_21:*
                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.6
88.4
87.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          774.5
764
764
761.5
759
759
759
759
759
759
759
759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                    OM protein
                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
No.
```

_		Ady14586 PRO polyp	Ady81119 Human bra	Aebil912 Human NM2	Aab60680 Bovine nu	Aab60681 Bovine nu	Aab14812 Human nm2		Aag79336 Human NM2		Aay07000 mm23-H2 p	Aag80282 Human NM2	Aag79337 Mature hu	Abu89707 Protein d	Adhl7091 Human nm2	Abm81902 Tumour-as	2 PRO	Adx05640 Cyclin-de	Ady14458 PRO polyp	Ady19693 PRO polyp
ADX05642	ADY19471	ADY14586	ADY81119	AEB11912	AAB60680	AAB60681	AAB14812	AA026423	AAG79336	AAG80280	AAY07000	AAG80282	AAG79337	ABU89707	ADH17091	ABM81902	ADP23162	ADX05640	ADY14458	ADY19693
σ	6	σ	0	0	4	4	m	Ŋ	Ŋ	4	7	4	S	9	ω	œ	æ	Φ	Φ	σ
152	152	152	152	152	152	152	176	176	176	152	152	152	152	152	152	152	152	152	152	152
			86.6	•	•		83.8		83.8	83.7		•	٠	٠	٠		•		83.2	•
759	759	759	759	759	755	754	734	734	734	733	729	729	729	729	729	729	729	729	729	729
25	56	27	28	29	30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

```
NM23; skin disease; intestinal disease; wound healing; vulnerary; ulcer; antitumour; gastrointestinal; dermatological; anti-inflammatory; tumour; antiulcer; nucleotide-diphosphate kinases; DNA-binding agent; psoriasis; transcription activating agent; Ras-GTPase regulator; Crohn's disease;
                                                                                                                                                                                                                                                                                                Regenbogen J;
                                                                                                                                                                                                                                                                                                Goppelt A,
                                                                                                                                                                                                                                                                    (SWIT-) SWITCH BIOTECH AG. (ETHZ-) ETH ZUERICH ETH ZENT HOENGGERBERG
                   AAG80281 standard; protein; 152 AA
                                                                                                                                                                                                                                                                                                Halle J,
                                                                                                                                                                                                                  22-FEB-2001; 2001EP-00103624.
                                                                                                                                                                                                                                      23-FEB-2000; 2000DE-01008330.
24-APR-2000; 2000US-0199312P.
                                                        (first entry)
                                                                            Murine NM23A protein.
                                                                                                                                                                                                                                                                                                 Werner S, Braun S,
                                                                                                                                                                                                                                                                                                                    WPI; 2001-490891/54
                                                                                                                                       NM23A; murine
                                                                                                                                                                             EP1127576-A1.
                                                                                                                                                          Mus musculus.
                                                         12-FEB-2002
                                                                                                                                                                                                 29-AUG-2001.
RESULT 1
```

Use of NM23 polypeptide and nucleic acid, for diagnosis, prevention, and treatment of skin and intestinal diseases, and in screening for

Claim 1; Page 21-22; 48pp; German.

therapeutic agents.

This invention describes a novel use of the NM23 protein family, for analysis, diagnosis, prevention and/or treatment of skin or intestinal diseases and/or wound healing and/or associated pathological disturbances. The products of the invention have vulnerary, antitumour, gastrointestinal, dermatological, anti-inflammatory and antiulcer activity. The NM23 protein family act as nucleotide-diphosphate kinases, DNA-binding and transcription activating agents and regulators of Ras-

```
ö
           them, and their encoding nucleic acids, or related vectors, transformed cells and antisense sequences, are used for analysis, diagnosis, prevention and/or treatment of skin and intestinal diseases (where associated with uncontrolled tissue growth or cell differentiation, particularly skin and intestinal tumours, also psoriasis, Crohn's disease and ulcers), wound healing and/or associated pathological alterations). They are also used to screen for agents that are potentially useful for treating these conditions. In vitro monitoring of NM23 protein expression in tissue samples provides an early diagnosis of disease. This sequence represents the murine NM23A protein described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                             61 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                              75 FIGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                 74
                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
antibodies (Ab) directed against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu C, Cao Y;
, Chen R, Wang ZW;
                                                                                                                                                                                                                                                                                                                                  1 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPP
                                                                                                                                                                                                                                                                                                                 15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                              91.1%; Score 798; DB 4; Length 152;
100.0%; Pred. No. 3e-82;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Asundi V, Zhou P, Xv
Wang D, Wang J, Zhang J, Ren F,
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                               DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM78984 standard; protein; 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-FEB-2000; 2000US-00496914.
27-AFR-2000; 2000US-00560875.
20-UIN-2000; 2000US-00598075.
19-UIL-2000; 2000US-00620325.
01-SEP-2000; 2000US-00663956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang D, Wanç
Wejhrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human protein SEQ ID NO 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-2000; 2000US-00693325
30-NOV-2000; 2000US-00728422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2001; 2001WO-US004098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-476283/51.
N-PSDB; AAK52117.
                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT, Liu C,
Ma Y, Zhao QA, 1
Xue AJ, Yang Y,
                                                                                                                                                                                                               Sequence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                                  nvention
                                                                                                                                                                                                                                                                                                                                                                                                                                               135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM78984;
                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
8888888888888888888
                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
ö
                                                                                      The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAW8329-AAM80302) that exhibit activity elating to cytokine, cell poliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 QPEFKPKQLEGTWANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytostatic; antitumour; lung small cell cancer antigen; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 OPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                          Query Match 90.8%; Score 795; DB 4; Length 223; Best Local Similarity 91.5%; Pred. No. 1.1e-81; Matches 150; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 CIQVGRNIHGSDSVESAEKEIGLWFRPEELVDYTSCAQNWIYE 223
                                                                                                                                                                                                                                                                                                          sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lodes MJ, Wang T, Mohamath R, Indirias CY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lung small cell carcinoma antigen #15.
                                                       Claim 20; Page 3984; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU69421 standard; protein; 178 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APR-2000; 2000US-0196780P.
21-JUN-2000; 2000US-0213361P.
01-SEP-2000; 2000US-0229763P.
05-SEP-2000; 2000US-022565P.
14-SEP-2000; 2000US-022565F.
19-DEC-2000; 2000US-022565P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-APR-2001; 2001WO-US011859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-010896/01
N-PSDB; AAS61861.
                                                                                                                                                                                                                                                                                                                                             Sequence 223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200177168-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU69421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

```
EMBL; CAA35621
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEB87772
셤
                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                         음
                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                        polynucleotides (I) and polypeptides (II) used in a method of detecting cancer in a patient. The method is optionally performed by utilising cancer in a patient. The method is optionally performed by utilising cancer in a patient. The method is optionally performed by utilising contacted with (III), where the biological sample from the patient is contacted with (III), detecting the amount of polynucleotide hybridised to (III) in the sample and comparing the amount of polynucleotide to a predetermined cut-off value and thereby determining cancer in a patient.

(I), (II) or antigen-presenting cells expressing (II) is useful for a timulating and/or expansion of the components under compositions to permit the stimulation and/or expansion of the cells. A composition comprising (I) is useful for stimulating an immune response in a patient and for inhibiting the development of a cancer especially lung cancer in a patient. An isolated T cell population is useful for removing tumour cells from the biological sample and for inhibiting the development of cancer in a patient. Adulg4907-Adul9431 represent novel tuman lung small cell cancer antigen amino acid sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                         74
                                                                               The invention relates to novel isolated lung small cell cancer antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                             15 QPEFKPKQLEGTMANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                             3 QPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Selectable marker; screening; diagnosis; liver disease; hepatotropic; gastrointestinal disease; liver cirrhosis; liver cancer; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
            Lung tumor polynucleotide and polypeptides useful in therapy and diagnosis of cancer especially lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.6%; Score 794; DB 5; Length 178; Best Local Similarity 91.5%; Pred. No. 1.1e-81; Matches 150; Conservative 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIQVGRNIIHGSDSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEA90110 standard; protein; 180 AA
                                                      Claim 2; Page 282; 295pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human NM23 protein, SEQ ID NO: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neoplasm; antigen; NM23 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INTE-) IND TECHNOLOGY RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-DEC-2004; 2004US-00013684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-DEC-2003; 2003TW-00136309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-AUG-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-444137/45
                                                                                                                                                                                                                                                                                                                                               Sequence 178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUN-2005
                                                                                                                                                                                                                                                                                                                     nvention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEA90110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iseng T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
AEA90110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
```

```
Analyzing differential protein expression associated with histopathologic features of breast disease, comprises detecting overexpression or underexpression of pool of proteins having Afadin, Aurora A, in breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 122
                                                                                                                                   The invention relates to novel biomarkers for liver diseases. The invention also relates to the use of an autoantigen screening method to identify biomarkers that can be used in detecting liver diseases such as liver cirrhosis and liver cancer. The present sequence is the human NM23 protein. This sequence is the autoantigen identified from cell lines using sera of patients with liver cirrhosis and liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
New biomarker for liver diseases comprising specific sequences, useful for developing kits for disgnosing liver cirrhosis or liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 QPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Breast tumor; breast disease; endocrine disease;
gynecology and obstetrics; neoplasm; prognosis; tumor marker;
DNA library; microarray; expression; NM23.
                                                                                                                                                                                                                                                                                                                                                                                                Score 794; DB 9; Length 180;
Pred. No. 1.1e-81;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tagett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 CIQVGRNIHGSDSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Debono
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IPSO-) IPSOGEN.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jacquemier J, Bertucci F, Birnbaum D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 42; 87pp; English.
                                                                                   Claim 1; SEQ ID NO 2; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEB87772 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human NM23, breast tumor marker.
                                                                                                                                                                                                                                                                                                                                                                                                      90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JAN-2004; 2004US-0537412P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-2005; 2005WO-IB000261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INST PAOLI CALMETTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-564257/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissues or cells.
                                                                                                                                                                                                                                                                                                                                                Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2005071419-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-OCT-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-2005
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAOL-)
```

```
process by process or particular breast tumores, e.g. breast carcinomas, comprising detecting the overexpression or underexpression of a pool of proceins in breast tissues or cells. The pool comprises all or part of a protein set comprising: afadin, aurora A, alpha-catenin, beta-catenin, BCL2, cyclin CDL, cyclin E, cytokeratin SA, cytokeratin SA, cytokeratin SE, angl, aurora B, BCRP1, rathepsin D, CDIO, CD4, CKI4, CCC, TACC3, rytokeratin G, cytokeratin 18, angl, aurora B, BCRP1, cathepsin D, CDIO, CD4, CKI4, CCC, cytokeratin SE, angl, aurora B, BCRP1, cathepsin D, CDIO, CD4, CKI4, CCC, cytokeratin SE, angl, aurora B, BCRP1, cathepsin D, CDIO, CD4, CKI4, CCC, cytokeratin SE, angl, aurora B, BCRP1, cathepsin D, CDIO, CD4, CKI4, CCC, cytokeratin SE, angl, aurora B, BCRP1, cathepsin D, CDIO, CD4, CKI4, CCC, cytokeratin SE, angl, aurora B, BCRP1, cathepsin D, CDIO, CD4, CKI4, CCC, cytokeratin SE, angl, aurora B, BCRP1, cathepsin D, CDIO, CD4, CKI4, CCC, cytokeratin SE, angl, such CCC, cytokeratin SE, angl, such CCC, cytokeratin SE, angl, such CCC, cytokeratin SE, cytokeratin SE, CCC, cytokeratin SE, CCC, cytokeratin SE, cytokeratin SE, CCC, cytokeratin SE, cytokeratin 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a patient can be based on the analysis of the differential protein expression profile. Breast cancers can be classified into prognostically relevant subclasses, and appropriate doses and/or schedule of chemotherapeutics and/or biopharmaceuticals and/or radiation therapy can be selected to circumvent toxicities in a patient. The method is also useful in assessing breast cancer heterogeneity and prognosis in patients with stage I, II or III disease. The present sequence is that of NM23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 KEHYVDLKDRPFFAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
The present invention provides a method for analyzing differential protein expression associated with histopathological features of breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 QPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 QPEFKPKQLEGTMANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.6%; Score 794; DB 9; Length 180; Best Local Similarity 91.5%; Pred. No. 1.1e-81; Matches 150; Conservative 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 CIQVGRNIIHGSDSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nm23-H1; tumour metastasis; cancer susceptibility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "encoded by CGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB14823 standard; protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human nm23 protein nm23-H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome 17q21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB14823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB14823
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

```
which is found on chromosome 17q21. Its coding sequence was isolated by searching a human fibroblast CDNA library for sequences similar to pnm23-M1. Nm23 proteins are involved in tumour metastasis, and this protein, its gene and antibodies can be used to determine an individual's susceptibility to cancer and the likelihood of tumour metastasis within that individual. This is possible using a number of methods, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 KEHYVDLKDRPFPAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 139
                                                                                                                                                                                                                                                                                         New nm23 monoclonal antibody which recognizes human nm23 protein, useful for detecting tumors which have low levels of nm23 protein and thus an increased ability to metastasize or be malignant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 QPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Northern blotting, nuclease protection assays, in situ hybridisation, immunohistochemical analysis and solid phase immunoassays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human nm23 protein; nm23-H1; nm23-H28; cancer; malignant potential; human tumour; genetic predisposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                   present sequence is the human nm23 protein nm23-H1, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.6%; Score 794; DB 3; Length 183; 91.5%; Pred. No. 1.1e-81; ive 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 CIQVGRNIHGSDSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 183
            /note= "putative first amino acid"
                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAO26422 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 6; 21pp; English.
                                                                                                        95US-00475684
                                                                                                                                    89US-00422801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein of the nm23-H1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 150; Conservative
                                                                                                                                                                                                                Steeg PS,
                                                                                                                                                                                                                                              WPI; 2000-531342/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
Misc-difference 33
                                                                                                                                                                                                                                                             N-PSDB; AAA70316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 183 AA;
                                                                                                      07-JUN-1995;
                                                                                                                                      18-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6423836-B1
                                                                                                                                                    11-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-2003
                                                                        11-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-2002.
                                            US6087117-A
                                                                                                                                                                                                                Liotta LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA026422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA026422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

ö

```
Active-site
                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE21724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                             음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                         The invention relates to an isolated polynucleotide molecule encoding a human nm23 protein comprising nm23-H1 having a sequence of 746 base pairs (bp) fully defined in the specification or nm23-H26 having a sequence of 670 bp fully defined in the specification. The polynucleotide molecule of the invention is useful as a diagnostic tool for detecting and/or determining RNA or DNA which can be employed to detect mNNA expression in cancer cells to aid in predicting the mailgnant potential of a human tumour. The DNA and the antibodies may also be used to detect abnormalities of DNAs in normal or cancer cells to aid in predicting the genetic predisposition for developing cancer. The human nm23 protein can be employed to produce mn23 antibodies. This sequence represents the nm23 HI protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                             122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140
                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                      New DNA molecule encoding a human nm23 protein useful for predicting the malignant potential of a tumor and the genetic predisposition for developing cancer, comprises nm23-H1 and nm23-H2s genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                      80
                                                                                                                                                                                                                                                                                                                                                                                                                 3 QPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                              63 KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 KEHYVDLKDRPFFAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NM23-H1; NM23-H2S; aggressiveness; metastatic potential; tumour; cancer susceptibility; early-onset familial breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                    Query Match 90.6%; Score 794; DB 5; Length 184; Best Local Similarity 91.5%; Pred. No. 1.1e-81; Matches 150; Conservative 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human NM23-H1 encoded from full length cDNA.
                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33. .184
/label= Mature NM23-H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG79335 standard; protein; 184 AA
                                                                 Steeg PS, Liotta LA
                                                                                                                                                                      Claim 1; Fig 6; 21pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00335948
91US-00806932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-2002 (first entry)
                                                                                       WPI; 2002-705184/76.
N-PSDB; AAL53614.
                                                                                                                                                                                                                                                                                                                                              Sequence 184 AA;
11-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6329198-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141
                                                                 King CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG79335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG79335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in AAG79335-38 show the related human proteins NM23-H1 and H2S. These proteins are products of different genes, with NM23-H1 being localised to chromosome 17. These proteins are used to predict aggressiveness (metastatic potential) of human tumours and in genetic tests for cancer susceptibility, diagnosis and prognosis, also for selection of treatment, e.g. susceptibility to early-onset familial breast cancer. Gene nm23 may contribute to tumourigenicity and alteration in its regulation may be an early stage in the metastatic cascade. Allelic or homozygous deletion of the gene is detected in some primary
                                                                                                                                                                                                                                                                                                                                                       New human NM23 protein, useful for diagnosis and prognosis of cancer, and assessment of aggressiveness and susceptibility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; kinase; enzyme; PKIN-19 protein; immune system disorder; anaemia; acquired immune deficiency syndrome; thymic hypoplasia; Crohn's disease; asthma; neurological disorder; epilepsy; Charcot-Marie-Tooth disease; AIDS; seizures; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; developmental disorder; Down's syndrome; gene therapy; protein therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QPQFKPKQLEGTWANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 QPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120. .168
/note= "Nucleoside diphosphate kinase active site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.6%; Score 794; DB 5; Length 184; 91.5%; Pred. No. 1.1e-81; ive 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16. .177 ________/label= Human_mature_PKIN-19_protein
                                                                                                                           USHE-) US DEPT SEC HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .15
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE21724 standard; protein; 177 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Col 23-24; 23pp; English.
                                                                                                                                                                                             Liotta LA;
89US-00422801.
91US-00806932.
95US-00475684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 91.5
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PKIN-19 protein.
                                                                                                                                                                                             King CR, Steeg PS,
                                                                                                                                                                                                                                                              WPI; 2002-121137/16
                                                                                                                                                                                                                                                                                                    N-PSDB; AAI72921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 184 AA;
18-OCT-1989;
11-DEC-1991;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
```

φ

Human prostatic carcinoma derived DNA SEQ ID 236 #4.

```
ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding such proteins. PKIN sequences of the invention are useful for diagnosing, treating or preventing disorders associated with aberrant expression of PKIN, particularly immune system disorders (e.g. acquired immune deficiency syndrome (AIDS), thymic hypoplasia, Crohn's disease, anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot-Marie-Tooth disease or seizures), cell proliferative disorders (e.g. cancers such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma), and developmental disorders (e.g. Down's syndrome). They are also used in gene therapy and protein therapy. The present sequence is human PKIN-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human kinases, useful for diagnosing, treating or preventing immune system disorders (e.g. Crohn's disease), neurological disorders (e.g. epilepsy), or cell proliferative disorders (e.g. cancers such as leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 EHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to human kinases (PKIN) and polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 EHYVDLKDRPFFAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 PPISSCD-TCTWANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLK 74
                                                                                                                                                                                                                                                                                                                  Bandman O, Nguyen DB, Walia NK, Hafalia AJA, Yao MG, Gandhi AR; Gururajan R, Ding L, Patterson C, Yue H, Baughn MR, Tribouley CM; Thornton M, Bliott VS, Lu Y, Ison CH, Au-Young J, Tang YT; Azimcai Y, Burrill JD, Marcus GA, Zingler KA, Lu DAM, Lal PG; Ramkumar J, Warren BA, Kearney L, Policky JL, Thangavelu K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 PAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 IQVGRNIIHGSDSVESAEKEIGLWFHPEELVDYTSCAONWIYE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 IQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.4%; Score 774.5; DB 5 90.2%; Pred. No. 1.8e-79; ive 4; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 74; Page 183-184; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR66938 standard; protein; 153 AA.
                                                                                                                                             08-SEP-2000; 2000US-0231357P.
14-SEP-2000; 2000US-0234902P.
22-SEP-2000; 2000US-0234902P.
29-SEP-2000; 2000US-0236499P.
06-OCT-2000; 2000US-0228389P.
13-OCT-2000; 2000US-0228389P.
                                                                                           31-AUG-2001; 2001WO-US027219
                                                                                                                                                                                                                                                                                 (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 90.2
nes 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-329769/36.
N-PSDB; AAD34316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 177 AA;
                   WO200218557-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or lymphoma).
                                                                                                                                31-AUG-2000;
                                                      07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                 Burford N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADR66938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR66938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  825525
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

```
This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular weight below 5000, preferably 300, that binds to the polypeptide; an aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the colypeptide, preferably humanised or human; an anti-idiotype, non-human complying a reporter group, cell toxin, immunostimulatory molecules and/or with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polymuleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, between normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated concer patients, or subjects at risk, were incubated second antibody; streptavidin-conjugated horseradish contextained with hemalum (blue). Malignant cells stained servond sumbrane and cytoplasmic staining was very strong, and propredice ago etained. ADR66954 represent the context also stained. ADR66954 represent the invalue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 TWANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRP
                                                                                                                                                                                                                                                                                                                                                                                                                                         Specht T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acids, and encoded proteins, from prostatic cancer tissue useful for diagnosis, treatment and in screening for specific binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Dahl E, Rosenthal A, Hermann K, Pilarsky C, Spech
Beckmann G, Bruemmendorf T, Kinnemann H, Roepcke S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 764; DB 8; Length 15
Pred. No. 2.2e-78;
3; Mismatches 6; Indels
                                       human; cytostatic; diagnosis; prostatic cancer; differential expression analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 1591; 1607pp; German.
                                                                                                                                                                                                                                                        27-FEB-2003; 2003DE-01009985.
14-MAY-2003; 2003DE-01022134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.2%;
94.1%;
                                                                                                                                                                                                                 22-FEB-2004; 2004WO-DE000433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 94.1
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staub E;
                                                                                                                                                                                                                                                                                                                                       DAHL E.
ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-653386/63
                                                                                                                                                                                                                                                                                                                  (HINZ/) HINZMANN B.
(DAHL/) DAHL E.
                                                                                                                                                                                                                                                                                                                                                                                                  PILA/) PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                HERMANN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 153 AA;
                                                                                                                                       WO2004076614-A2
                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmitt A, Xinzhong L,
                                                                                                                                                                            10-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                           (ROSE/)
(HERM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agents.
```

ö 73

ò

(first entry)

02-DEC-2004

```
29-MAY-2002
                                                                                                                            nvention.
                                                                                                                                                                                                                                                                                                                                                  134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB99909;
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB99909
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                              유
                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer. Or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection broatances involves a binding assay, any compounds that bind are substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonucleotides, consistent farmer against the polypeptide; an expanic molecule of molecular aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide; an anti-idictype, non-human (monoconal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polynucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, cancer by differential expression analysis, using DNA microarrays.

Cancer by differential and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from
                                        FFAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHH 120
 9
 TMANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRP
                            FFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for specific binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht
Beckmann G, Bruemmendorf T, Kinnemann H, Roepcke S;
                                                                                                                                                                                                                                                                 ŧ.
                                                                                                                                                                                                                                                                 Human prostatic carcinoma derived protein SEQ ID 236
                                                                                                                                                                                                                                                                                             human; cytostatic; diagnosis; prostatic cancer;
                                                                                 134 SDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                 121 SDSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 153
                                                                                                                                                                                Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 631; 1607pp; German.
                                                                                                                                                                                                                                                                                                             differential expression analysis.
                                                                                                                                                                               ADR66040 standard; protein; 153
                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-2004; 2004WO-DE000433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-FEB-2003; 2003DE-01009985.
14-MAY-2003; 2003DE-01022134.
                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAHL E.
ROSENTHAL A.
HERMANN K.
PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinzhong L, Staub E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-653386/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HINZMANN B.
                                                                                                                                                                                                                                                                                                                                                                 WO2004076614-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hinzmann B,
                                                                                                                                                                                                                                       02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                            10-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schmitt A,
                                                                                                                                                                                                            ADR66040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HINZ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ROSE/)
(HERM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PILA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DAHL/)
                                                                                                                                                      RESULT 11
                                                                                                                                                                   ADR66040
                                                                                                                                                                                  8
                                                     셤
                                                                                 ઠ
                                                                                                      g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 FFTGLVXXMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 FraglukymhsgpvvamvmeglnvvktgrvmlgetnpadskpgtirgdfciqvgRniihg 120
prostatic cancer patients, or subjects at risk, were incubated sequentially with anti-human CD4 murine monoclonal antibodies; blotinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained atrongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65805-ADR66954 represent the polymucleotide and polypeptide sequences used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to nucleoside diphosphate kinase 19.47 (ABB99909) and nucleic acids encoding it (ABG77987). The protein has a malecular weight of 19.47 kD. The invention also relates to a method for the recombinant production of the protein, an antagonist of the protein, and the use of the protein, gene and antagonist in therapeutic applications. Nucleoside diphosphate kinase 19.47 can be used in the treatment of a variety of diseases such as tumours, embryonic development disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide diphosphate kinase 19.47; recombinant production; gene therapy; tumour; cancer; embryonic development disorder; paralysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TMANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 TMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptide-protein 19.47 containing nucleoside diphosphate kinase activity site characteristics and polynucleotide for encoding it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.2%; Score 764; DB 8; Length 153; 94.1%; Pred. No. 2.2e-78; ive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 SDSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 27 (Disclosure); 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BODE-) BODE GENE DEV CO LTD SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide diphosphate kinase 19.47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB99909 standard; protein; 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-2000; 2000CN-00125776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-OCT-2000; 2000CN-00125776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-644397/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; tumous
cytostatic; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABQ77987
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CN1351016-A.
```

us-10-074-694-3.rag

SXXXX

8 g ò 셤 ò 셤

```
The present sequence represents human nm23-H1 protein. The specification describes a method for the diagnosis of metastatic potential of a carcinoma in a patient. The method comprises obtaining a sample of chromosomal DNA from the tumour of the subject, and analysing the sample of chromosomal DNA from the tumour of the subject, and analysing the sample of chromosomal DNA for the presence or absence of a human nm23-H1 allele. The absence of a human nm23-H1 allele subject has previously had or currently has breast carcinoma, non-small cell lung carcinoma or kidney carcinoma. The metastatic potential is due to allelic deletions in the human nm23 quer, nm23-H1. The method can also be used for the diagnosis of colorectal carcinoma or neuroblastoma in patients who have had or currently have such carcinoma
                  61 PAGLVKYMHSGPVVAMVWEGLINVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 FTGLVKXMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCLQVGRNIHGS 134
 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                               Mouse; NM23-1 protein; diagnosis; metastatic potential; carcinoma; human; nm23-H1 allele; allelic deletion; colorectal carcinoma; neuroblastoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosis of metastatic potential of carcinoma - comprises analysis of chromosomal DNA sample from the patient's tumour for presence or absence of human nm23-H1 allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 759; DB 2; Length 152;
Pred. No. 8.3e-78;
3; Mismatches 6; Indels
                                                                                          DSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steeg PS
                                                                         DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liotta LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Col 3-6; 22pp; English.
                                                                                                                                                                                                     Ź
                                                                                                                                                                                                     standard; protein; 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87US-00107098.
89US-00422801.
90US-00528713.
91US-00775081.
94US-00190562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-00406005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.1%;
Matches 143; Conservative
                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leone A, Bevilacqua G,
                                                                                                                                                                                                                                                                                                             Human nm23-H1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-311392/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV38413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 152 AA;
                                                                                                                                                                                                                                                                           11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-1991;
02-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-OCT-1989;
24-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                        US5753437-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-1998
 75
                                                                                                         121
                                                                                                                                                                                                                                         AAW62505;
                                                                         135
                                                                                                                                                                                                     AAW62505
                                                                                                                                                                  RESULT 14
                                                                                                                                                                                      AAW62505
                                                                                                                                                                                                       셤
                                 셤
                                                                         ð
                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding this human nm23 protein is useful for detecting mRNA expression in cancer cells and for helping predict the malignant potential of a human tunnour. This nm23 protein is useful for raising antibodies for detecting tumours having low levels of mm23 protein and thus an increased ability to undergo metastasis or be malignant. See also
                                                                                                                                                                                                                                       64 EHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFC 123
                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                    74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
paralysis. The present sequence represents nucleoside diphosphate kinase 19.47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NM23 protein, deoxyribonucleic acid and antibodies - used to predict metastasis, malignant potential and aggression of human tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                    16 PPISSCD-TGTWANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFWQASEDLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRPP
                                                                                                                                                                4 PAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLK
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                              ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                            Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.6%; Score 759; DB 2; Length 152; 94.1%; Pred. No. 8.3e-78; ive 3; Mismatches 6; Indels
                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                  135 IQVGRNIIRGSDSVESAEKEIGLWPHPEELVDYTSCAQNWIYE 177
                                                                                                                                                                                                                                                                                                             124 IQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                              13;
                                                                                          DB 5;
                                                                                        Score 761.5; DB 5
Pred. No. 5.3e-78;
4; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human nm23; tumours; cancer; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR11903 standard; protein; 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liotta LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-00422801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89US-00422801
                                                                                          86.9%;
89.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USDC ) US SEC OF COMMERCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steeg PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1991-148689/20
                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human nm23 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ11721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 152 AA;
                                                      Sequence 177 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUL-1991
                                                                                                                              Matches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9105793-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR11903;
                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ11721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              King
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                         AAR11903
```

ö

Gaps . 0 74 9

В

ò

```
Search completed: December 16, 2005, 16:43:38 Job time: 141.333 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences given in AAG79335-38 show the related human proteins NM23-H1 and H2S. These proteins are products of different genes, with NM23-H1 abing localised to chromosome 17. These proteins are used to predict aggressiveness (metastatic potential) of human tumours and in genetic tests for cancer susceptibility, diagnosis and prognosis, also for selection of treatment, e.g. susceptibility to early-onset familial breast cancer. Gene nm23 may contribute to tumourigenicity and alteration in its regulation may be an early stage in the metastatic cascade. Allelic or homozygous deletion of the gene is detected in some primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTGLVKYMHSGPVVAMVWEGLAVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human NM23 protein, useful for diagnosis and prognosis of cancer, and assessment of aggressiveness and susceptibility.
61 FAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                      NM23-H1, NM23-H2S, aggressiveness, metastatic potential; tumour; cancer susceptibility; early-onset familial breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.6%; Score 759; DB 5; Length 152; 94.1%; Pred. No. 8.3e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                             DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSVESAEKEIGLWFHPEELVDYTSCAONMIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USHE-) US DEPT SEC HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                  AAG79338 standard; protein; 152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Col 21-24; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steeg PS, Liotta LA;
                                                                                                                                                                                                                                                                                                                                                                                                                      89US-00422801.
91US-00806932.
95US-00475684.
                                                                                                                                                                                                                                                                                                                                                                                            99US-00335948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.19
Matches 143; Conservative
                                                                                                                                                                                            21-AUG-2002 (first entry)
                                                                                                                                                                                                                          Mature human NM23-H1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-121137/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAI72921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 152 AA;
                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                  US6329198-B1
                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                       11-DEC-1991;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               King CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                  AAG79338;
                                                                                                        RESULT 15
                                                                                                                      AAG79338
                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
```

This Page Blank (uspto)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

December 16, 2005, 16:31:59; Search time 24.5346 Seconds (without alignments) 650.999 Million cell updates/sec

Title: Perfect score:

US-10-074-694-3 876 1 QSQPAVKPCHLKGTWANSER......WFQPEELVEYKSCAQNWIYE 166 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES	
Result No.	Score	% Query Match	Length	DB	ΙD	Description
-	876	100.0	166	7	A46557	nucleoside-diphosp
73	779		152	7	N	nucleoside-diphosp
9	759	9.98	152	٦	A33386	nucleoside-diphosp
4	729	83.2	152	~	A49798	nucleoside-diphosp
ß	720	82.2	152	~	A38369	nucleoside-diphosp
9	719	82.1	152	~	S29241	nucleoside-diphosp
7	611	69.7		~	801908	nucleoside-diphosp
80	547.5	62.5		N	I39074	nucleoside-diphosp
6	528.5	60.3		N	T21354	hypothetical prote
10	519.5	59.3		~	JC4359	nucleoside-diphosp
11	514.5	58.7		7	S33170	nucleoside-diphosp
12	514	58.7		N	T01877	nucleoside-diphosp
13	513	58.6		~	T08909	hypothetical prote
14	510.5	58.3	148	7	T14183	nucleoside-diphosp
15	510	58.2		7	T50459	nucleoside-diphosp
16	500.5	57.1		~	T07042	nucleoside-diphosp
17	499.5	57.0		~	S24165	nucleoside-diphosp
18	495.5	56.6		7	T17131	nucleoside-diphosp
19	494	56.4		~	560363	nucleoside-diphosp
20	492	56.2	_		S37889	nucleoside-diphosp
21	491	56.1	-	-	T39099	nucleoside-diphosp
22	490.5	56.0	-		S31444	•
23	487.5	55.7	"		S43330	nucleoside-diphosp
24	478	54.6	-	7	A49547	nucleoside-diphosp
25	476	54.3	149		S76467	nucleoside-diphosp
56	475.5	4.	144	~	~	nucleoside-diphosp.
27	472	53.9	231	~	258	nucleoside-diphosp
28	461	ς.	152	~	21	nucleoside-diphosp
29	460	52.5	220	7	B49547	nucleoside-diphosp

nucleoside-diphosp nucleoside-diphosp	nucleoside diphosp nucleoside-diphosp nucleoside diphosp	nucleoside-diphosp nucleoside diphosp nucleoside diphosp	nucleoside diphosp probable nucleosid nucleoside diphosp	nucleoside-diphosp nucleoside diphosp	hypothetical prote nucleoside-diphosp nucleoside diphosp
S52785 G69345	593936 S28226 D69666	531446 H84271 E89925	AI1687 C71116 AI1315	D69132 D75044	D90164 H64457 F75266
000	9000	N 00 10	000	0 0	000
151	233 149	148 161 149	147	151	138 140 191
52.2	51.5	48.1 47.3 47.0	46.1 45.9	44.3	41.3 41.1 40.9
456	451 445	421 414 124	404 404 202	388	362 360 358
330	ን E E E	3 9 9 7 9 7 9 9 9 9 9 9 9 9 9 9 9 9 9 9	8 6 6 8 6 6	4 4 5 1 0	4 4 4 6 4 8

ALIGNMENTS

RESULT 1
A46557 nucleoside-diphosphate kinase (EC 2.7.4.6) - mouse (fragment) N,Alternate names: differentiation-inhibiting factor; tumor metastasis inhibitor NM23
C;Species: Mus musculus (house mouse) C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 05-Oct-2004 C:Arresion: AAK557. R33386. T52807. JN0281
R;Steed Street S.; Bevilacqua, G.; Kopper, L.; Thorgeirsson, U.P.; Talmadge, J.B.; Liotta, L.
9. Mart. Cancer fine. 60, 200-204, 1500 A;Title: Evidence for a novel gene associated with low tumor metastatic potential. A;Reference number: A46557; MUID:88155671; PMID:3346912
A;Accession: A46557 A:Starus: preliminary
A; Modern Lype: mRNA , benique: 1-16 cgm.
A; Cross-references: UNIPROT: P15532; UNIPARC: UP1000016CF64; GB: M35970; NID: 9200066; PIDN:
A;Note: the authors translated the codon 195 for residue 153 as 191 R;Rosengard, A.M.; Krutzsch, H.C.; Shearn, A.; Biggs, J.R.; Barker, E.; Margulies, I.M.K.
Nature 342, 177-180, 1989 A;Title: Reduced Nm23/Awd protein in tumour metastasis and aberrant Drosophila developmer
A;Reference number: A33386; MUID:90044071; PMID:2509941 A:Accession: R33386
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
ARC: UPI000000188F
R;Leone, A.; Flatow, U.; King, C.R.; Sandeen, M.A.; Margulles, I.M.; Llotta, L.A.; Steeg, Cell 65, 25-35, 1991
A; Title: Reduced tumor incidence, metastatic potential, and cytokine responsiveness of nn
A; Kelerence number: 132007; Morb: 3131535, Khirb: 2013033 A; Accession: 152807
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mkNA A;Residues: 15-166 <res></res>
A;Cross-references: UNIPARC:UPI00000188F; GB:M65037; NID:g200068; PIDN:AAA63391.1; PID:
Riochem Blophys. Res. Commun. 182, 984, 1992
A; Title: Identity of a differentiation inhibiting factor for mouse myeloid Leukemia Cells A: Reference number: JN0281; MUID:92171977; PMID:1311576
A;Accession: JN0281
A; Residues: 19-21;23-25; M';54-55, R';57-59, E';61,63,'Q';'YI';78-98;100-103;105-113;115-
A;CIOSS-references INI-PARC:UFLOUNDISSER'S UNI-PARC:UFLUUULS/SSC; UNI-PARC:UFLUUULS/SSC; UNI-PARC:UFLUUULS/VS; 70R: INITDARC:UFLUUULS/SSC; UNI-PARC:UFLUUULS/SSC; UNI-PARC:UFLUUUULS/SSC; UNI-PARC:UFLUUULS/SSC; UNI-PARC:UFLUUULS/SS
A;Experimental source: myeloid leukemia cell A;Experiment Bource: myeloid leukemia cell C;Comment. This factor is Nm21/nucleoside diphosohate kinase (EC 2.7.4.6) involved in tun
C;Genetics:
Ajene: nmz.s CjSuperfamily: nucleoside diphosphate kinase CjSuperfamily: hiding: hexamer: phosphohistidine; phosphoprotein; phosphotransferase; f
F_i 29-33/Region: ATP binding #status predicted F_i 132/Active site: His (phosphohistidine intermediate) #status predicted

us-10-074-694-3.rpr

N

8

```
Hum. Genet. 93, 63-66, 1994
A,Title: Isolation and characterization of the human genomic locus coding for the putativ A,Reference number: 845376; MUID:94095204; PMID:8270257
A,Stetus: preliminary
                                                                                                                                                                                                               A;Residues: 1-152 <DOO>
A;Residues: 1-152 <DOO>
A;Cross-references: UNIPARC:UPI0000112099; EMBL:X75598; NID:g468541; PIDN:CAA53270.1; PII
R;Gilles, A.M.; Presecan, E.; Vontca, A.; Lascu, I.
J. Biol. Chem. 266, 8784-8789, 1991
A;Title: Nucleoside diphosphate kinase from human erythrocytes. Structural characterizatj
A;Reference number: A39838; MUID:91224972; PMID:1851158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G.M.; Reynold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Note: mutant sequence shown (tumor 10) was extracted from NCBI backbone; wild type seqn.
A,Note: sequence extracted from NCBI backbone (NCBIN:124581, NCBIP:124584)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Accession: A43931
A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
A, Fesidues: 7-18,40-49,89-94 (HAI>
A, Cross-references: UNIPARC; UPI000004BCA0; UNIPARC: UPI00001726A5
A, Note: sequence modified after extraction from NCBI backbone
A, Note: sequence modified after extraction from NCBI backbone
A, Note: sequence modified after extraction from NCBI backbone
A, Note: Sequence modified after extraction from NCBI backbone
Cancer Res. 53, 717-720, 1993
A, Title: Mutation in the nm23 gene is associated with metastasis in colorectal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: UNIPARC:UPI0000112099
R;Hailat, N.; Keim, D.R.; Melhem, R.F.; Zhu, X.X.; Eckerskorn, C.; Brodeur, G.M.; Reyno, C.lin. Invest. 88, 341-345, 1991
A;Title: High levels of p19/mm23 protein in neuroblastoma are associated with advanced A;Reference number: A43931; MUID:91277302; PMID:2056128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Cross-references: GDB:127965; OMIM:156490
A;Map position: 17q21-17q22
A;Introns: 43/1; 77/2; 114/2
C;Superfamily: nucleoside diphosphate kinase
C;Keywords: ATP binding; blocked amino end; hexamer; phosphohistidine; phosphoprotein; F;15-19/Region: ATP binding #status predicted
F;118/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nm23-H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A49798

mucleoside-diphosphate kinase (EC 2.7.4.6) nm23-H2 - human

mucleoside-diphosphate kinase (EC 2.7.4.6) nm23-H2 - human

mylternate names: c-myc transcription factor PuF; tumor metastasis inhibitor () Species: Homo sapiens (man)

C; Date: 03-May-1994 #sequence_revision 12-Mar-1999 #text_change 05-Oct-2004

C; Accession: A49798; B39838; I59581

R; Stahl, J.A.; Rosengard, A.M.; Porter, L.; King, C.R.; Steeg, P.S.

Cancer Res. 51, 445-449, 1991

A; Title: Identification of a second human nm23 gene, nm23-H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MANCERTFIAIKPDGVQRGLVGGIIKRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGPRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 86.6%; Score 759; DB 1; Length 15 Il Similarity 94.1%; Pred. No. 5.2e-65; 143; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-86,'SAYKLAGTLYMAVILWRVQRRRSACGFTLRNW' <WAN>
A;Cross-references: UNIPARC:UP100001726A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 143; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: GDB:NME1; nm23-H1
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A39838
A;Molecule type: protein
A;Residues: 1-152 <GIL>
                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A56882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: seqn
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-152 <ROS>
.A;Cross-references: UNIPROT:P15531; UNIPARC:UP10000112099; GB:X75598; NID:g468541; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleoside-diphosphate kinase (EC 2.7.4.6) isoform beta - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C;Accession: A45208
R;Shimada, N.; Ishikawa, N.; Munakata, Y.; Toda, T.; Watanabe, K.; Kimura, N.
Biol. Chem. 286 22833-2589, 1993
A;Title: A second form (beta isoform) of nucleoside diphosphate kinase from rat. Isolati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleoside-diphosphate kinase (EC 2.7.4.6) nm23-H1g - human
NyAlternate names: nm23-H1g protein; probable metastatic suppressor nm23-H1
C;Species: Homo aaplans (man)
C;Decies: Homo aaplans (man)
C;Accession: A33386; S45376; A39838; A43931; A56882; B43931; C43931
R;Rosengard, A.M.; Krutzsch, H.C.; Shearn, A.; Biggs, J.R.; Barker, E.; Margulies, I.M.K
A;Title: Reduced Nm23/Awd protein in tumour metastasis and aberrant Drosophila developme
A;Reference number: A33386; MUD:90044071; PMID:2509941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: A45208
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-152 < SHI>
A;Cross-references: UNIPROT:Q05982; UNIPARC:UPI000012FE91; GB:D13374; NID:g286231; PIDN:A;Experimental source: skeletal muscle
A;Note: sequence extracted from NCBI backbone (NCBIP:124170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: nucleoside diphosphate kinase
C;Keyworda: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F;15-19/Region: ATP binding #status predicted
F;118/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                              61 LLKEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRG 120
                                                                                                                                                                                                                                                                                                                               LIKEHYTDIKORPFFTGLVKYMISGPVVANVMEGLNVVKTGRVMLGETNPADSKPGTTRG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                    1 QSQPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASED
                                                                                                                                                                                                        QSQPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                      Gaps
                                                                                                      ..
0
                                       Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                           121 DFCIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DFCIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                  Indels
                                    Score 876; DB 2;
Pred. No. 4.1e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 779; DB 2;
Pred. No. 6.4e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                  0; Mismatches
                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.9%;
96.7%;
                                                                     Best Local Similarity 100.0
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.73
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135
                                       Query Match
                                                                                                                                                                    ठ
                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

ď

```
A,Cross-references: UNIPARC:UPI000012FE93; GB:M55331; GB:J05588; NID:g205661; PIDN:AAA416 R.18hikawa, N.; Shimada, N.; Munakata, Y.; Watanabe, K.; Kimura, N. J. Biol. Chem. 267, 14366-14372, 1992
A,Fittle: Isolation and characterization of a gene encoding rat nucleoside diphosphate kir A,Reference number: A42967; MUID:92332552; PMID:1321145
A,Accession: A42967
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-152 <1SH>
A,Residues: 1-152 <1SH>
A,Residues: L-152 <1SH>
A,Cross-references: UNIPARC:UPI000012FE93
A,Octoss-references: UNIPARC:UPI000012FE93
                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: nucleoside diphosphate kinase
C; Superfamily: horamer; phosphohistidine; phosphoprotein; phosphotransferase; r
F;15-19/Region: ATP binding #status predicted
F;118/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: nucleoside diphosphate kinase
Kswywodas APP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase; I
F;15-19/Region: ATP binding #status predicted
F;118/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross_references: UNIPROT: Q01768; UNIPARC: UPI0000003EFD; EMBL: X68193; NID: 953353; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the second mouse nm23/NDP kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleoside-diphosphate kinase (EC 2.7.4.6) - fruit fly (Drosophila melanogaster)
N;Alternate names: K-pn protein; killer-of-prune protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FPGLVKYMNSGPVVAMVWEGLANVVKTGRVWLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 MANSERTFIAIKPDGVQRGLVGBIIKRFBQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleoside-diphosphate kinase (EC 2.7.4.6) B - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MANDERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVANKFLRASEBHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.2%; Score 720; DB 2; Length 152; 88.2%; Pred. No. 2.7e-61; ive 11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.1%; Score 719; DB 2; Length 15:
88.2%; Pred. No. 3.3e-61;
iive 11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Accession: $29241
R;Urano, T.; Takamiya, K.; Furukawa, K.; Shiku, H.
FBES Lett. 309, 358-362, 1992
A;Title: Molecular cloning and functional expression of A;Reference number: $29241; WUID:92387389; PMID:1325378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.24
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.23
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-152 <URA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S29241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S01908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleoside-diphosphate kinase (EC 2.7.4.6) precursor - rat
Cispecies: Rattus norvegicus (Norway rat)
Cibate: 28-Jun-1991 #sequene revision 28-Jun-1991 #text_change 05-Oct-2004
CiAccession: A41849; A38369; A42967
R;Hemmerich, S.; Yarden, Y.; Pecht, I.
Biochemiatry 31, 4574-4579; 1992
A;Title: A cromogyloate binding protein from rat mast cells of a leukemia line is a nucl
A;Reference number: A41849; MUID:92256389; PMID:1316151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-152 <HEM-
A;Cross-references: UNIPROT:P19804; UNIPARC:UPI000012FE93
A;Cross-references: UNIPROT:P19804; UNIPARC:UPI000012FE93
B;Kimura, N.; Shimada, N.; Nomura, K.; Watanabe, K.
J. Biol. Chem. 265, 15744-15749; 1990
A; Title: Isolation and characterization of a cDNA clone encoding rat nucleoside diphosph
A;Reference number: A38369; MUID:9036877; PMID:2168422
A;Accession: A38369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPARC:UP10000112864
R;Postel, E.H.; Berberich, S.J.; Flint, S.J.; Ferrone, C.A.
Science 261, 478-480, 1993
A;Title: Human c-myc transcription factor PuF identified as nm23-H2 nucleoside diphospha
A;Reference number: 159581; MUID:93324921; PMID:8392752
                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosadues: 1-152 <STA>
A;Crosa-references: UNIPROT:P22392; UNIPARC:UP10000112864; GB:X58965; NID:g35069; PIDN:C
K;Gilles, A.M.; Presecan, B.; Vonica, A.; Lascu, I.
B;Gilles, A.M.; Presecan, B.; Vonica, A.; Lascu, I.
A;Title: Nucleoside diphosphate kinase from human erythrocytes. Structural characterizat
A;Reference number: A39838; MUID:91224972; PMID:1851158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reaidues: 1-152 <RES>
A;Cross-references: UNIPARC:UPI0000112864; GB:L16785; NID:9349475; PIDN:AAA60228.1; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase; F;15-19/Region: ATP binding #status predicted F;118/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 83.2%; Score 729; DB 2; Length 15 Best Local Similarity 90.1%; Pred. No. 3.7e-62; Matches 137; Conservative 9; Mismatches 6; Indels
                    A, Reference number: A49798; MUID:91105674; PMID:1988104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSVKSAEKEISLWFQPEELVEYKSCAONWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Map position: 17q21-17q22
C,Superfamily: nucleoside diphosphate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GDB:128020; OMIM:156491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein A;Residues: 1-152 <GIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-152 <KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: A41849
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                    A; Accession: B39838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: I59581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB: NME2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
```

õ 셤 ò 요 ð

```
A;Residues: 1-153 <GHO>
A;Residues: 1-153 <GHO>
A;Cross-references: UNIPROT:P48817; UNIPARC:UPI000012FE9C; GB:U18906; NID:g619942; PIDN:J
C;Comment: This enzyme is a pivotal enzyme in the synthesis of nucleotide triphosphates c
de triphosphates, supplying GTP for GTP-binding proteins and a role in signal transductic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Keywords: ÅTP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase; F;13-17/Region: ATP binding #status predicted
F;106/Active site: Arg #status predicted
F;119/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Aclecule type: DNA
A;Molecule type: DNA
A;Residues: 1-153 <WILL>
A;Cross-references: UNIPROT:Q93576; UNIPARC:UPI000007F609; EMBL:Z79754; PIDN:CAB02101.1;
A;Experimental source: clone F25H2
C;Genetics:
A;Gene: CESP:F25H2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: JG4359
R;Ghosh, I.; Raghavan, N.; FitzGerald, P.C.; Scott, A.L.
R;Ghosh, I.; Raghavan, N.; FitzGerald, P.C.; Scott, A.L.
A;Title: Nucleoside diphosphate kinase from the parasitic nematode Brugia malayi.
A;Reference number: JC4359; MUID:96069592; PMID:7590340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 MANS-ERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRP 73
                                                                                                                                                                                                                                                                           C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C,Accession: T21354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Date: 08-Jan-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleoside-diphosphate kinase (EC 2.7.4.6) - nematode (Brugia malayi)
C;Species: Brugia malayi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 60.3%; Score 528.5; DB 2; Best Local Similarity 65.4%; Pred. No. 4.6e-43; Matches 100; Conservative 23; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.3%; Score 519.5; DB 2; 62.7%; Pred. No. 3.3e-42; ive 26; Mismatches 30;
                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 DSVKSAEKEISLWFQPEELVEYKS-CAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 DAVDSANREIAHWFKQEEINDYASPFINSWVYE 153
                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, September 1996
                                                                         C; Superfamily: nucleoside diphosphate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: nucleoside diphosphate kinase
                                                                                                                                                                                                                                               hypothetical protein F25H2.5 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: Z19411
A;Accession: T21354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: JC4359
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 1
A; Introns: 18/2; 49/3
                                                                                                                                                                                                                                                                                                                                                                 R;Wilkinson, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: ndk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                           σ
                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JC4359
                                                                                                                                                                                                                          T21354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
C;Species: Drosophila melanogaster
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S01908
R;Biggs, J; Tripoulas, N.; Hersperger, E.; Dearolf, C.; Shearn, A.
Genes Dev. 2, 1333-1343, 1988
A;Title: Analysis of the lethal interaction between the prune and killer of prune mutatis
A;Reference number: S01908
A;Reference number: S01908
A;Residues: 1-153 <-BIG>
A;Residues: 1-153 <-BIG>
A;Cross-references: UNIPROT:P08879; UNIPARC:UPI00000011C4; EMBL:X13107; NID:g7634; PIDN:
C;Genetics:
A;Gene: awd
A;Cross-references: Flybase:FBgn0000150
A;Map position: 3 100C-D
C;Superfamily: nucleoside diphosphate kinase
C;Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F;16-20/Region: ATP binding #status predicted
F;16-20/Region: ATP binding #status predicted
F;10-20/Region: ATP binding #status predicted
F;119/Active site: His (phosphohistidine intermediate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: 139074
R:Venturelli, D.D.; Martinez, R.R.; Calabretta, B.B.
Proc. Natl. Acad. Sci. U.S.A. 92, 7435-7439, 1995
A;Title: Overexpression of DR-nm23, a protein encoded by a member of the nm23 gene famil A;Reference number: 139074; MUID:95365382; PMID:7638209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ы
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: nucleoside diphosphate kinase
C;Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F;32-36/Region: ATP binding #status predicted
F;134/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A/Accession: I39074
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Rociecus: prye: mRNA
A/Rociecus: 1-168
A/Rosicus: GBS: NME3
A/Rosicus: GBS: NME3
A/Rosicus: 16413-16413
C/Superfamily: nucleoside diphosphate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 TGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 PGLVNYMNSGPVVPMYWEGLNVVKTGRQMLGATNPADSLPGTIRGDFCIQVGRNIIHGSD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleoside-diphosphate kinase (EC 2.7.4.6) DR-nm23 - human
N;Alternate names: DR-nm23 protein; non-metastatic cell-expressed protein 3
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ANKERTFIMVKPDGVQRGLVGKIIERFEQKGFKLVALKFTWASKELLEKHYADLSARPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 ERTFIAIKPDGVQRGLVGBIIKRFBQKGFRLVGLKFLQASBDLLKBHYTDLKDRPFFTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 ANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 69.7%; Score 611; DB 2; Length 15
Best Local Similarity 76.2%; Pred. No. 6.5e-51;
Matches 115; Conservative 16; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.5%; Score 547.5; DB 2; 66.2%; Pred. No. 8.1e-45; tive 32; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 SVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
Les 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

유

ò

원

ò

ò

ò

ö

g ð g

Š

```
R.; Bancroft, I.; Mewes, H.W.; Maye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q8LAH8; UNIFARC:UPI00000ABF3A; EMBL:AL078468; GSPDB:GN00062; A;Experimental source: cultivar Columbia; BAC clone T32A16
C;Genetics:
A;Experimental source: cultivar Columbia; BAC clone F25124
C;Genetics:
A;Gene: ATSP:F8M12.12; ATSP:F25124.220; ndpk3
A;Map position: 4
A;Introns: 28/1; 75/1; 87/3; 104/3; 160/3; 198/2
C;Superfamily: nucleoside diphosphate kinase
C;Seywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase; F;99-103/Region: ATP binding #status predicted
F;123/Active site: Lys #status predicted
F;202/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 TGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 TGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypochetical protein T32A16.70 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08909
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewe aubmitted to the Protein Sequence Database, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114183
nucleoside-diphosphate kinase (BC 2.7.4.6) - common sunflower
C;Species: Helianthus annuus (common sunflower)
C;Species: Helianthus annuus (common sunflower)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14183
R;Grayburn, W.S.; Vick, B.A.
submitted to the EMBL Data Library, September 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 ANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 ANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 58.7%; Score 514; DB 2; Best Local Similarity 61.3%; Pred. No. 1.9e-41; Matches 92; Conservative 27; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 58.6%; Score 513; DB 2; Similarity 62.7%; Pred. No. 2.4e-41, 94; Conservative 24; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 4
A;Introns: 28/1; 74/1; 86/3; 103/3; 159/3; 197/2
C;Superfamily: nucleoside diphosphate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 SVKSAEKEISLWFQPEELVEYKSCAQNWIY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 GPETAKDEISLWFKPQELVSYTSNSEKWLY 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 SVKSAEKEISLWFQPEELVEYKSCAQNWIY 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::|: ||||||:||||| | | |: |||
GPETAKDEISLWFKPEELVSYTSNAEKWIY 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: T08909
A;Molecule type: DNA
A;Residues: 1-237 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: ATSP: T32A16.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T08909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1.238 <BEV>
A;Cross-references: UNIPARC:UPI000012FE87; EMBL:AL049525; GSPDB:GN00062; ATSP:F25I24.22d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:O49203; UNIPARC:UPI000012FE87; EMBL:AF080118; NID:g3513725; A;Experimental source: cultivar Columbia
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Note: submitted to the EMBL Data Library, April 1993
C;Superfamily: nucleoside diphosphate Kinase
K;Reywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F;13-17/Region: ATP binding #status predicted
F;116/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-149 <FI2>
A;Cross-references: UNIPROT:P47922; UNIPARC:UPI000012FE7F; EMBL:X71388; NID:g296173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: S46513; S33170 —
R,Finan, P.M.; White, I.R.; Redpath, S.H.; Findlay, J.B.C.; Millner, P.A.
Blant Mol. Biol. 25, 59-67, 1994
A;Title: Molecular cloning, sequence determination and heterologous expression of A;Reference number: S46513; MUID:94272014; PMID:8003697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                              78 LVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSV 137
                                                                                                                                      133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleoside-diphosphate kinase (EC 2.7.4.6) - Arabidopsis thaliana N.Alternate names: protein F25124.220; protein F8M12.12 C.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004 C.Accession: T01877; T04296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Pieum Bativum (garden pea)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                    FFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 SERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleoside-diphosphate kinase (EC 2.7.4.6) - garden pea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.7%; Score 514.5; DB 2;
ilarity 64.4%; Pred. No. 9.7e-42;
Conservative 21; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                134 SDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                         |||: |||:||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R,Madsen, C.; Graves, T.; Cotton, M.; Modde, T. submitted to the EMBL Data Library, July 1998 A;Description: The sequence of A. thaliana F8M12. A;Accession: T01877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|| |||:||| || || || ESANKEIALWF-PEGAANWESSLHSWIYE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 KSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reference number: Z15261; Accession: T04296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: DNA
Residues: 1-238 <MAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Accession: S46513
                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
```

셤 δ පු 8 임 ö

144

φ

```
Search completed: December 16, 2005, 16:39:05 Job time: 25.5346 secs
               A.Accession: T14183
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Wolecule type: mRNA
A.Wolecule: 1-148 «GRA>
A.Residues: 1-148 «GRA>
A.Cross-references: UNIPROT:096559; UNIPARC:UP1000012FEAB; EMBL:U72142; NID:g1619957; PI
C.Function:
A.Bescription: catalyzes transfer of the gamma-phosphate group from ATP to nucleoside di
cid synthesis, UTP for polysaccharide synthesis, CTP for lipid synthesis and GTP for pro
by modulating GTP levels
C.Superfamily: nucleoside diphosphate kinase
C.Superfamily: phosphotistidine; phosphotrein; phosphotransferase; pyrimidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleoside-diphosphate kinase (EC 2.7.4.6) [validated] - Neurospora crassa Nicontains: protein kinase (EC 2.7.4.6) [validated] - Neurospora crassa Cispeciase: Neurospora crassa (Cispeciase: Neurospora crassa (Cispeciase: Neurospora erassa (Cispeciase: Neurospora erassa (Cispeciase: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004 (Cispeciase: 09-Jun-2004 #sequence_revision 09-Jun-2000 #text_change (N.; Hasunuma, K. Eur. J. Blochem. 266, 709-714, 1999 A;Title: Isolation and characterization of Neurospora crassa nucleoside-diphosphate kina A;Reference number: 225071; MUID:20050582; PMID:10583364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Note: ndk-1
C;Function: <NDK1>
A;Description: EC 2.7.4.6 [validated, MUID:20050582]; phosphorylates nucleoside diphosph
C;Function: <PKIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9UUY8; UNIPARC:UPI000012FEB8; EMBL:D88148; NID:g5771347; C;Genetics:
A;Introns: 7/2; 112/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 VKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 PFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIH 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EQTFIMIKPDGVQRGLVGEIIGRFEKKGFTLKGLKLLTVDQAFAEKHYADLSAKPFFNGL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASED--LLKEHYTDLKDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BRIFIAIKPDGVQRGLVGBIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPFFTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Description: phosphorylates proteins in vitro (validated, MUID:20050582) A,Note: acts as a signal transducer by phosphorylating proteins C,Superfamily: nucleoside diphosphate kinase C,Keywords: phosphoprotein; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 58.2%; Score 510; DB 2; Length 154; Best Local Similarity 60.4%; Pred. No. 2.7e-41; Matches 93; Conservative 27; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.3%; Score 510.5; DB 2; Length Best Local Similarity 65.5%; Pred. No. 2.3e-41; Matches 97; Conservative 18; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 GSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: T50459
A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
A;Residues: 1-154 <OGUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 SAEKEISLWFQPEELVEYKSCAQNWIYE 166
Reference number: Z17907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     연 , +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
```

Mon Dec 19 07:55:15 2005

nucleoside-diphosp nucleoside diphosp nucleoside diphosp nucleoside diphosp probable nucleosid nucleoside diphosp nucleoside diphosp nucleoside diphosp nucleoside diphosp nucleoside diphosp nucleoside diphosp nucleoside diphosp

T52586 F83856 D69666 S31446 S28226 H16271 A116871 C71116 D710315 D7103

2231 1447 12430 12430 1244 1244 1240 1251 138

ALIGNMENTS

RESULT 1

nucleoside diphosp nucleoside-diphosp nucleoside-diphosp

nucleoside-diphosp

```
December 16, 2005, 16:31:59 ; Search time 22.4654 Seconds (without alignments) 650.999 Million cell updates/sec
                                                                                                                                                                                            1 MANLERTFIAIKPDGVQRGL.........WFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       results predicted by chance to have a
                                                                                                                                                                                                                                                                                                             283416
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                            hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                           283416 segs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                        Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                             US-10-074-694-5
803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the number
             Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR 80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is t
score greater
and is derived
                                                                                                                                                                                                                                                                                                                                                                                             Post-processing:
                                                                                                                                                                                                                                                                                                             Total number of
                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         803
794
732
729
720
620
                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
```

				RESULT 1
length: 0 length: 2000000000	0000			A49798 nuclearide-diphosphate kinase (EC 2.7.4.6) nm23-H2 - human N.N.Learate names. C.mvo transcription factor DHF. tumor metastasis inhibitor nm23-H2
Minimum Match Maximum Match Listing first		0% 100% 45 summaries		C.Species: Homo sapiens (man) C.Date: 03-May-1994 #sequence_revision 12-Mar-1999 #text_change 05-Oct-2004 C.Accession: A49798; B39838; T59581
PI				ריאי; פרפפט,
1: pir1:* 2: pir2:*				A;Title: Identification of a second numan nmz3 gene, nmz3-nz. A;Reference number: A49798; MUID:91105674; PMID:1988104
				A.Accession: A49798 A.Status: preliminary
	4			A Molecule type: mRNA A Molecule type: mRNA A mocidator 1152 ceman
is the number of r ater than or equal	qual	s the number or results predicted by chance to mave a er than or equal to the score of the result being printed,	ce to mave a It being printed,	A; CESTAGNES: I-1-2. SIMPROT: P22392; UNIPARC: UPI0000112864; GB: X58965; NID: 935069; PIDN:
rived by analysis of	818	of the total score distribution.	bution.	R;Gilles, A.M.; Presecan, E.; Vonica, A.; Lascu, I. I Biol Chem 266 8784-8789 1991
		SUMMARIES		A;Title: Nucleoside diphosphate kinase from human erythrocytes. Structural characteriza.
ر م			•	A;Reference number: A39838; MUID:91224972; PMID:1851158 A:Accession: R39838
Length	DB	ID	Description	A;Status: preliminary
	- 1			A; Molecule type: protein
	~	A49798	nucleoside-diphosp	A;Residues: 1-152 (GIL)
98.9 152	. v	A38369 S29241	nucleoside-aipnosp nucleoside-diphosp	A) LIGHEL TELEFICIES UNIFARCITIONS (A) FERFORE C.A. R: PASKEL E. H.: Berberich. S.J.: Flint. S.J.: Ferrone, C.A.
	1 (1	327241 A45208	nucleoside-diphosp	Science 261, 478-480, 1993
		A46557	nucleoside-diphosp	A,Title: Human c-myc transcription factor PuF identified as nm23-H2 nucleoside diphosph
		A33386	nucleoside-diphosp	A; Reference number: 159581; MUID: 93324921; PMID: 8392752
-		801908		A; Accession: 159581
		T21354	hypothetical prote	A;SCETUR: LITRIBIALCE LION GB/EMBU/DUBU
66.8 168		1390/4	nucleoside-diphosp	A.Molecute / free / fre
		T50459	nucleoside-diphosp	A; Cross-references: UNIPARC: UPI0000112864; GB: L16785; NID: 9349475; PIDN: AAA60228.1; PID
		T14183	nucleoside-diphosp	C;Genetics:
-		833170	nucleoside-diphosp	A; Gene: GDB: NMEZ
		537889		A;Cross-references: GDB:1128020; OMIM:150491
62.9 237 62.8 148	N 0	T08909 S24165	nypornerical prore	A;wap posttuni: vq-1-1rq-2 C:Superfamily: nucleoside diphosphate kinase
		T01877	nucleoside-diphosp	C; Kerwords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
		843330	nucleoside-diphosp	F,15-19/Region: ATP binding #status predicted
		860363	nucleoside-diphosp	F;118/Active site: His (phosphohistidine intermediate) #status predicted
		T07042	nucleoside-diphosp	Occasional top Ob. Cante phil in D. Length 152.
61.6 149		71/131 S31444	micleograe-diphosp	Similarity 100.0%; Pred. No. 1.8e-71;
59.7 149		S76467	nucleoside-diphosp	tive 0
-	7	T39099	nucleoside-diphosp	•
-	~	S47974	nucleoside-diphosp	(GLVGEI I KRFEQKGFRLVAMKFLKASEEHLKQH I I DLKUKFF
Π,	~ 0	G69345	nucleoside-diphosp	n
	7 C	A4954/ B49547	nucleoside-diphosp	
56.3 152	1 (1)	D3337 T51612	nucleoside-diphosp	Qy 61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120

ö

Gaps

.; 0

120

9 9

g ò 셤

```
A,Accession: S29241
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Cross-references: UNIPROT:Q01768; UNIPARC:UPI0000003EFD; EMBL:X68193; NID:g53353; PIDN
C,Superfamily: uncleoside diphosphate Kinase
C,Superfamily: uncleoside diphosphate Kinase
C,Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F,15.19/Region: ATP binding #status predicted
F,118/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C.Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C.Accession: AA508
R.Shimada, N.; Ishikawa, N.; Munakata, Y.; Toda, T.; Watanabe, K.; Kimura, N.
J. Biol. Cham. 268, 2583-2589, 1993
A; Title: A second form (beta isoform) of nucleoside diphosphate kinase from rat. Isolat:
A; Reference number: A45208; MUID:93155067; PMID:8381409
A; Accession: A45208
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-152 < SHI>
A; Cross-references: UNIPROT: Q05982; UNIPARC: UPI000012FE91; GB:D13374; NID:g286231; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase; F;15-19/Region: ATP binding #status predicted
F;118/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleoside-diphosphate kinase (EC 2.7.4.6) - mouse (fragment)
N,Alternate names: differentiation-inhibiting factor; tumor metastasis inhibitor NM23
C;Specias: Mus musculus (house mouse)
C;Date: 03-Mar-1994 #sequence revision 03-Mar-1994 #text_change 05-Oct-2004
C;Accession: A46557; B33386; Ī52807; JN0281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FSGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCLQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFC1QVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 732; DB 2; Length 152;
Pred. No. 1.7e-64;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                 Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleoside-diphosphate kinase (EC 2.7.4.6) isoform beta - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: skeletal muscle
A;Note: sequence extracted from NCBI backbone (NCBIP:124170)
   A; Reference number: S29241; MUID: 92387389; PMID: 1325378
                                                                                                                                                                                                                                                                                                  Score 793; DB 2; Le
Pred. No. 1.8e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                98.8%; bcc...
98.0%; Pred. No. ...
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: nucleoside diphosphate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.2%;
90.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.1%
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                A MARGA CALLER AND ADDRESS OF CALL OF DECURSOR - rat CSPECIAS RATIONS OF CALL OF CALLER OF CALCAGO CALLORD OF CALCAGO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: S29241
Kybrano, T.; Takamiya, K.; Furukawa, K.; Shiku, H.
FEBS, Lett. 309, 358-562, 1992
A;Title: Molecular cloning and functional expression of the second mouse nm23/NDP kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-Jul-2004
FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCLQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MANLERTFIAIKPDGVORGLVGEIIKRFEOKGFRLVAMKFLRASEEHLKOHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleoside-diphosphate kinase (EC 2.7.4.6) B - mouse C;Species: Mus musculus (house mouse) C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 794; DB 2;
Pred. No. 1.4e-70;
                                                                                                                                                   DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSVESAEKEIGLWFKPEELIDYKSCAHDWVYE
                                                                                                      DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.9%;
98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 98.0
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                     61
```

9

Gaps . 0

> ð 셤 ò 셤 ò 임

رد'

```
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Cross-references: UNIPROT:P15531; UNIPARC:UP10000112099; GB:X75598; NID:g468541; PIDN:
R;Dooley, S.; Seib, T.; Engel, M.; Theisinger, B.; Janz, H.; Piontek, K.; Zang, K.D.; We
R;Dooley, S.; Seib, T.; Engel, M.; Theisinger, B.; Janz, H.; Piontek, K.; Zang, K.D.; We
A;Title: Isolation and characterization of the human genomic locus coding for the putat;
A;Reference number: 845376; MUID:94095204; PMID:8270257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UP10000112099; EMBL:X75598; NID:g468541; PIDN:CAA53270.1; PI R;Gilles, A.M.; Presscan, E.; Vonica, A.; Lascu, I. d. Biol. Chem. 266, 8784-8789, 1991
A;Title: Nucleoside diphosphate kinase from human erythrocytes. Structural characterizat A;Reference number: A39838; MUID:91224972; PMID:1851158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: A39838
A;Molecule type: protein
A;Residues: 1-152 <GIL>
A;Cross-references: UNIPARC:UPI0000112099
Ciff. Inrest: 88, 341-345, 1991
A;Title: High levels of p19/nm23 protein in neuroblastoma are associated with advanced the A;Reference number: A43931; MUID:91277302; PMID:2056128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A;Residues: 7-18;40-49;89-94 <HAI>
A;Cross-references: UNIPARC:UPI00004BCA0; UNIPARC:UPI00001726A4; UNIPARC:UPI00001726A5
A;Note: sequence modified after extraction from NCBI backbone
R;Mang, L.; Patel, U.; Ghosh, L.; Chen, H.C.; Banerjee, S.
Cancer Res. 53, 717-720, 1993
A;Title: Mutation in the nm23 gene is associated with metastasis in colorectal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hexamer; phosphohistidine; phosphoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-86,'SAYKLAGTLYMAVILWRVQRRRSACGFTLRNW' <WAN>
A;Cross-references: UNIPARC:UPI00001726A6
A;Cross-references blown (tumor 10) was extracted from NCBI backbone; wild type
A;Note: mutant sequence extracted from NCBI backbone (NCBIN:124581, NCBIP:124584)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S01908
nucleoside-diphosphate kinase (EC 2.7.4.6) - fruit fly (Drosophila melanogaster)
N;Alternate names: K-pn protein; killer-of-prune protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .., ..... mucation in the nm23 gene is associated with metastasis in colorectal A;Reference number: A56882; MUID:93153759; PMID:7916650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: nucleoside diphosphate kinase
Keywords: ATP binding; blocked amino end; hexamer; phosphohistidine; pl
F;15-19/Region: ATP binding #status predicted
F;118/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 720; DB 1; Lengtu ...
Pred. No. 2.5e-63;
Pred. No. 2.5e-63;
                       A; Reference number: A33386; MUID: 90044071; PMID: 2509941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:127965; OMIM:156490
A;Map position: 17q21-17q22
A;Introns: 43/1; 77/2; 114/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.7%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: GDB:NME1; nm23-H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <DOO>
                                                                               A; Accession: A33386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A43931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              유
R;Steeg, P.S.; Bevilacqua, G.; Kopper, L.; Thorgeirsson, U.P.; Talmadge, J.E.; Liotta, I. J. Natl. Cancer Inst. 80, 200-204, 1988
A;Title: Evidence for a novel gene associated with low tumor metastatic potential.
A;Reference number: A46557; MUD:88155671; PMID:3346912
A;Accession: A46557
A;Accession: A46557
A;Accession: A46557
A;Accession: A46557
A;Accession: A46557
A;Accession: A166
A;Title: Note: the authors translated the codon TGG for residue 163 as Tyr
B;Rosengard, A.M.; Krutzsch, H.C.; Shearn, A.; Biggs, J.R.; Barker, B.; Margulies, I.M.;
A;Note: the authors translated the codon TGG for residue 163 as Tyr
B;Rosengard, A.M.; Krutzsch, H.C.; Shearn, A.; Biggs, J.R.; Barker, B.; Margulies, I.M.;
A;Title: Reduced Nm23/Awd protein in tumour metastasis and aberrant Drosophila developme
A;Reference number: A3386; MUID:90044071; PMID:2509941
A;Reference number: B3386
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 15-166
A;Status: 15-166
A;Status: 15-186
A;Cross-references: UNIPARC:UPI000000188F
B;Leone, A.; Flatcow, U.; King, C.R.; Sandeen, M.A.; Margulies, I.M.; Liotta, L.A.; Steeg
Cell 65, 25-35, 1991
A;Title: Reduced tumor incidence, metastatic potential, and cytokine responsiveness of n
A;Reference number: 152807; MUID:91191558; PMID:2013093
A;Accession: 152807; MUID:91191558; PMID:2013093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 15-166 <RES
A;Cross-references: UNIPARC:UPI00000188F; GB:M65037; NID:9200068; PIDN:AAA63391.1; PID:
R;Okabe-Kado, J.; Kasukabe, T.; Honma, Y.; Hayashi, M.; Henzel, W.J.; Hozumi, M.
Biochem: Biochys: Res. Commun. 182, 987-994, 1992
A;Title: Identity of a differentiation inhibiting factor for mouse myeloid leukemia cell
A;Reference number: JN0281; MUID:92171977; PMID:1311576
A;Accession: JN0281
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleoside-diphosphate kinase (EC 2.7.4.6) nm23-H1g - human
N;Alternate names: nm23-H1g protein; probable metastatic suppressor nm23-H1
C;Species: Home sapiens (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 05-Oct-2004
C;Accession: A33386; S45376; A39838; A43931; A56882; B43931; C43931
C;Rocengard, A.M.; Krutezsch, H.C.; Shearn, A.; Biggs, J.R.; Barker, E.; Margulies, I.M.K
Nature 342, 177-180, 1989
A;Title: Reduced Nm23/Awd protein in tumour metastasis and aberrant Drosophila developme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                급
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: nucleoside diphosphate kinase
Kreywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
F;29-33/Region: ATP binding #status predicted
F;132/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Comment: This factor is Nm23/nucleoside diphosphate kinase (EC 2.7.4.6) involved Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNVPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 729; DB 2; Length 16
Pred. No. 3.7e-64;
9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Experimental source: myeloid leukemia cell
C, Comment: This factor is Nm23/nucleoside di
C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 90.8%;
Best Local Similarity 90.1%;
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
```

Be

ö 09 9

Gaps

ö

Page

H

64 81

```
A;Cross-references: UNIPROT:P48817; UNIPARC:UPI000012FE9C; GB:U18906; NID:g619942; PIDN C;Comment: This enzyme is a pivotal enzyme in the synthesis of nucleotide triphosphates de triphosphates, supplying GTP for GTP-binding proteins and a role in signal transduct: C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                         a member of the nm23 gene famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Map position: 16q13-16q13
C.Superfamily: nucleoside diphosphate kinase
C.Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase;
E,32-36/Region: ATP binding #status predicted
F,134/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase; F13-17/Region: ATP binding #status predicted F;106/Active site: Arg #status predicted F;110/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-168 <RES>
A;Cross-references: UNIPROT:Q13232; UNIPARC:UPI0000149FCF; EMBL:U29656; NID:g1051255;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleoside-diphosphate kinase (EC 2.7.4.6) - nematode (Brugia malayi)
C;Species: Brugia malayi
C;Species: Brugia malayi
C;Species: Brugia malayi
C;Accession: JG4359
R;Ghosh, I.; Raghavan, N.; FitzGerald, P.C.; Scott, A.L.
Gene 164, 261-266, 1995
A;Title: Nucleoside diphosphate kinase from the parasitic nematode Brugia malayi.
A;Reference number: JC4359; MUID:96069592; PMID:7590340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MANL-ERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRP 59
                                                                                                                                                           Nalternate diphosphate kinase (EC 2.7.4.6) DR-nm23 - human NiAlternate names: DR-nm23 protein; non-metastatic cell-expressed protein 3 Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Ja-May.1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
Cisacession: I39074
Riverturelli, D.D.; Martinez, R.R.; Calabretta, B.B.
Proc. Natl. Acad. Sci. U.S.A. 92, 7435-7439, 1995
A;Title: Overexpression of DR-nm32, a protein encoded by a member of the nm: A;Reference number: I39074; MUID:95365382; PMID:7638209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERTF1A1KPDGVQRGLVGE11KRFEQKGFRLVAMKFLRASEEHLKQHY1DLKDRPFFPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 534.5; DB 2;
Pred. No. 4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.8%; Score 536.5; DB 2;
64.9%; Pred. No. 2.9e-45;
iive 33; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.4%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || :||:|||: :||: :| | :|| | sARREIALWFRADELLCWEDSAGHWLYE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: nucleoside diphosphate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GDB:5215169; OMIM:601817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB: NME3; DR-nm23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-153 <GHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: 139074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ഗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: ndk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F25H2.5 - Caenorhabditis elegans
C;Species: Caet-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21354
R;Wilkinson, J.
A;Reference number: Z19411
A;Reference number: Z19411
A;Reference number: Z19411
A;Reference number: Z19411
A;Reference number: Z1941
A;Refer
C;Species: Drosophila melanogaster
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S01908
R;Bidgs, J.; Tripoulas, N.; Hersperger, E.; Dearolf, C.; Shearn, A.
Genes Dev. 2, 1333-1343, 1988
A;Title: Analysis of the lethal interaction between the prune and killer of prune mutatis A;Reference number: S01908, MUID:89079007; PMID:2849580
A;Reference number: S01908
A;Rocession: S01908
A;Cross-references: UNIPROT:P08879; UNIPARC:UPI00000011C4; EMBL:X13107; NID:g7634; PIDN: C;Genetics:
A;Gene: awd
A;Cross-references: FlyBase:FBgn0000150
A;Map position: 3 100C-D
C;Superfamily: nucleoside diphosphate kinase
C;Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase; F;16-20/Region: ATP binding #status predicted
F;16-20/Region: ATP binding #status predicted
F;119/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 PGLVNYMNSGPVVPMVWEGLNVVKTGRQMLGATNPADSLPGTIRGDFCIQVGRNIIHGGD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANKERTFIMVKPDGVQRGLVGKIIERFEQKGFKLVALKFTWASKELLEKHYADLSARPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FPSLIEYMSSGPVVAMVWQGLDVVKQGRSMLGATNPLASAPGTIRGDFCIQTGRNICHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 77.2%; Score 620; DB 2; Length 15 Best Local Similarity 77.5%; Pred. No. 1.6e-53; Matches 117; Conservative 14; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 69.4%; Score 557.5; DB 2; Best Local Similarity 68.6%; Pred. No. 2.2e-47; Matches 105; Conservative 21; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSVKSAEKEISLWFKPEELVDYKS-CAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 SVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٦9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
```

ò 셤 ò g ò g 1;

g

ð 셤 ò ద

ò

9

ծ

ò

```
by modulating GTP levels
C;Superfamily: nucleoside diphosphate kinase
C;Keywords: ATP binding; phosphohistidine; phosphoprotein; phosphotransferase; pyrimidi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleoside-diphosphate kinase (EC 2.7.4.6) [validated] - yeast (Saccharomyces cerevisia. NyAlternate names: protein YKL057w; protein YKL033 (S.Speciess: Saccharomyces cerevisiae (S.Speciess Saccharomyces cerevisiae (S.Speciess Saccharomyces cerevisiae (S.Speciess) Saccharomyces cerevisiae (S.Speciess) S37889; S44519; JN0754; S39174 #text_change 09-Jul-2004 (S.Accession: S37889; S44519; JN0754; S39174 #text_change 09-Jul-2004 submitted to the Protein Sequence Database, March 1994 #xeference number: S37872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: 837889
A;Molecule type: DNA
A;Residues: 1-153 «RAS>
A;Cessidues: 1-153 «RAS>
A;Cessidues: 1-154 "NIPROT:P36010; UNIPARC:UP10000037234; EMBL:228067; NID:g486092; PIIA;Experimental source: strain $288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-149 <FI2>
A;Cross-references: UNIPROT:P47922; UNIPARC:UPI000012FE7F; EMBL:X71388; NID:9296173; Pli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: ATP binding; hexamer; phosphohistidine; phosphoprotein; phosphotransferase; F;13-17/Region: ATP binding #status predicted F;116/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleoside-diphosphate kinase (EC 2.7.4.6) - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 22.Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: 846513; 833170
R;Finan, P.M.; White, I.R.; Redpath, S.H.; Findlay, J.B.C.; Millner, P.A.
Bjant Mol. Biol. 25, 55-77, 1994
A;Title: Molecular cloning, sequence determination and heterologous expression (A;Reference number: 846513; MUID:94272014; PMID:8003697
                                                                                                                                                                                                                                                                                                                                                                                                                                           LVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGSDSV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 VKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVK 124
                                                                                                                                                                                                                                                                                                                3 EQTFIMIKPDGVQRGLVGEIISRFEKKGFYLKGLKFVNVERAFAEKHYADLSAKPFFSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 ERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFFPGL
                                                                                                                                                                                                                                                                     4 LERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFFPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                     ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
H
                                                                                                                                      Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Note: submitted to the EMBL Data Library, April 1993
C,Superfamily: nucleoside diphosphate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 509.5; DB 2;
Pred. No. 1.1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                      DB 2;
                                                                                                                                  63.6%; Score 510.5; DB 2; 63.8%; Pred. No. 8.7e-43; ive 22; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.4%; Score 50.5..,
63.5%; Pred. No. 1.1e-
tive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||:||| ||| || : :: | | ::||
ESAKKEIGLWF-PEGVANWSSSLHPWIYE 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 KSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SANKEIALWF-PEGAANWESSLHSWIYE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 SAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 63.58
Best Local Similarity 63.58
Conservative
                                                                                                                                  Query Match
Best Local Similarity 63.8%
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S46513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.; Accession Y.; Yoshida, Y.; Ichimura, K.; Aoyagi, C.; Yabe, N.; Hasunuma, K.

Bur. J. Biochem. 266, 709-714, 1999
A; Title: Isolation and characterization of Neurospora crassa nucleoside-diphosphate kind
A; Reference number: 225071; MUID:20050582; PMID:10583364
A; Accession: T50459
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-154 <0GU>
A; Cross-references: UNIPROT:Q9UUY8; UNIPARC:UPI000012FEB8; EMBL:D88148; NID:g5771347; PI
C; Genetics:
A; Introns: 7/2; 112/3
A; Note: ndk-1
C; Function: ADRI>
A; Description: EC 2.7.4.6 [validated, MUID:20050582]; phosphorylates nucleoside diphosph
A; Description: EC 2.7.4.6 [validated, MUID:20050582]; phosphorylates nucleoside diphosph
A; Description: EC 2.7.4.6 [validated, Muid: Validated, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: UNIPROT: Q96559; UNIPARC: UPI000012FEAB; EMBL: U72142; NID: 91619957; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Description: catalyzes transfer of the gamma-phosphate group from ATP to nucleoside di cid synthesis, UTP for polysaccharide synthesis, CTP for lipid synthesis and GTP for pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFFPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIH 118
                                                                                                                                             61 PFNDLVGYMSSGPVIAMVWEGLDVVKQARQMLGATNPLNSMPGTIRGDFSIQTGRNIVHG 120
                                                                                                      FPPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEH--LKQHYIDLKDR 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleoside-diphosphate kinase (EC 2.7.4.6) - common sunflower
C;Species: Helianthus annuus (common sunflower)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contains: protein kinase
Species: Neurospora crassa
Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
   T50459
nucleoside-diphosphate kinase (EC 2.7.4.6) [validated] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.4%; Score 525; DB 2;
62.3%; Pred. No. 3.4e-44;
iive 25; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 GSDSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Accession: T14183
R;Grayburn, W.S.; Vick, B.A.
submitted to the EMBL Data Library, September 1996
A;Reference number: Z17907
A;Accession: T14183
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                   121 SDSLPSAEREITHWFKPEELCEWSSATATWVYE 153
                                                                                                                                                                                                                                            120 SDSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Molecule type: mRNA
A, Residues: 1-148 cGRA>
A, Cross-references: UNIPR
C, Function: Catalyzes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: T50459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                              유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
```

nucle

ŏ

```
December 16, 2005, 16:39:06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Job time : 23.4654 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         completed:
                                                                                                                                                                                                                                                                                                                                                                               205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search
                                                                                                                                                               셤
                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                          g
                                                                          ò
R; Rasmussen, S. W.
Yeast 10, 69-74, 1994

A; Title: Sequence of a 20.7 kb region of yeast chromosome XI includes the NUP100 gene, a rp in addition to seven ORFs with weak or no significant similarity to known proteins.
A; Reference number: S44513
A; Accession: S44519
A; Status: nucleic acid sequence not shown
A; Residues: 1-153 cRA2>
A; Cross-references: UNIPARC:UP10000037234; EMBL:X75780; NID:g433625; PIDN:CAA53407.1; PI
R; Pukuchi, T.; Nikawa, J.; Kimura, N.; Watanabe, K.
Gene 129, 141-146, 1993
A; Title: Isolation, overexpression and disruption of a Saccharomyces cerevisiae YNK gene
A; Recension: UNO754; MUD:93328116; PMID:8392963
A; Title: Isolation, overexpression and disruption of a Saccharomyces cerevisiae YNK gene
A; Recension: UNO754
A; Mulber 123 cFUX
A; Residues: 1-153 cFUX
A; Residues: 1-15 cFUX
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T12A16.70 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08909
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; May submitted to the Protein Sequence Database, May 1999
A;Accession: T08909
A;Accession: T08909
A;Molecule type: DNA
A;Accession: T08909
A;Molecule type: DNA
A;Accession: T08909
A;Accession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 VKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 ERTFIAVKPDGVQRGLVSQILSRFEKKGYKLVAIKLVKADDKLLEQHYAEHVGKPFFPKM 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 ERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFFPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 62.9%; Score 505; DB 2; Length 15. Best Local Similarity 61.5%; Pred. No. 3.1e-42; Matches 91; Conservative 28; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 62.9%; Score 505; DB 2; Best Local Similarity 62.0%; Pred. No. 5.4e-42; Matches 93; Conservative 25; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 4
A;Introns: 28/1; 74/1; 86/3; 103/3; 159/3; 197/2
C;Superfamily: nucleoside diphosphate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAEREINLWFKKEELVDWESNOAKWIYE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene: ATSP:T32A16.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
62 PGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSD 121
                             122 SVKSAEKEISLWFKPEELVDYKSCAHDWVY 151
                                                                                                                                              ::|: |||||||||||| | | | :|
GPETAKDEISLWFKPEELVSYTSNAEKWIY 234
```

```
(LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAX40201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9904265-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O'hare M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY07000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  old LJ,
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mature hu
Protein d
Human nm2
Tumour-as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRO polyp
PRO polyp
Tumor met
Human nm2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine NM
Human pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mm23-H2 p
Human NM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein o
Human NM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human nuc
Human MDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human pro
Human gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO polyp
Cyclin-de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine nu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovine Murine 1
                                                                                         ; Search time 126.667 Seconds (without alignments) 527.255 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                           1 MANLERTFIAIKPDGVQRGL..........NFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abu 39337 N
Abu 3937 N
Abu 3937 N
Abu 3937 N
Abu 393162 N
Adv14458 N
Adv14659 N
Adv16693 N
Adv16693 N
Adv16631 N
Adv16631 N
Adv16623 N
Adv16623 N
Adv16623 N
Adv16623 N
Adv16623 N
Adv16623 N
Adv16624 N
Adv166624 N
Adv16664 N
Adv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aay07000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aam78984
                                                                                                                                                                                                                                                                                                          2443163
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                            2443163 segs, 439378781 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                            December 16, 2005, 16:31:59
                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG80282
AAG79337
ABU89707
ADH17091
ABM81902
ADP23162
ADX05640
ADX19693
AEA89623
AAB14812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG26423
AAG79336
AEA90109
ABP51330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG80283
ADR66920
ADR66022
ABO58327
AABC681
AABC680
AAG80281
                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      geneseqp2001s:*
geneseqp2002s:*
geneseqp2003bs:*
geneseqp2004s:*
geneseqp2004s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     geneseqp1980s:*
geneseqp1990s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     geneseqp2000s:*
                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Geneseq 21:*
1: geneseqp198
                                                                                                                                                           US-10-074-694-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                          Minimum DB s
Maximum DB s
                                                                                                                                                                                              Seguence:
                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
```

	Aae21724 Aau69421	AAE21724 AAU69421	លល	177	89.7 89.7	720	444
Human pro Human pro	Adr66938 Adr66040	ADR66938 ADR66040	യ യ	153 153	89.7	720	
_	Aeb11912	AEB11912	Q	152	89.7	720	
Human	Ady81119	ADY81119	0	152	89.7	720	
	Ady14586	ADY14586	σ	152	89.7	720	
PRO polyp	Ady19471	ADY19471	0	152	89.7	720	
Cyclin-de	Adx05642	ADX05642	σ	152	89.7	720	
Human pro	Adw08712	ADW08712	σ	152	7.68	720	
Novel bro	Adu06448	ADU06448	œ	152	89.7	720	
PRO polyp	Adp23235	ADP23235	00	152	89.7	720	
Human PRO	Adp54261	ADP54261	80	152	89.7	720	_
Tumour-as	Abm81903	ABM81903	æ	152	89.7	720	
Human PRO	Ado19200	ADO19200	80	152	89.7	720	
Antipsori	Adn05777	ADN05777	æ	152	89.7	720	_
Human PRO	Ad182817	ADL82817	Ф	152	89.7	720	_
Novel hum	Adf76437	ADF76437	7	152	89.7	720	_
Mature hu	Aag79338	AAG79338	ហ	152	89.7	720	_
Human nm2	Aaw62505	AAW62505	N	152	89.7	720	
Human nm2	Aar11903	AAR11903	~	152	89.7	720	

ALIGNMENTS

```
AAY07000 standard; protein; 152 AA.
                                                                                 (first entry)
                                                                                                                         mm23-H2 protein sequence
```

Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer; prostate cancer. 98WO-US014679

97US-00896164. 97US-0061599P. 97US-0061765P. 97US-00948705. 97GB-00021697.

Chen Y, Gout I; Stockert E, Gure A, Cher Pfreundschuh M, Tureci O, Scanlan MJ, Obata Y, WPI; 1999-132448/11. New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers.

Example 8; Page 787; 787pp; English.

The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically

~

```
ö
                                                                                                                                                                                                                                                                                                                                                                                PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                    61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of NM23 polypeptide and nucleic acid, for diagnosis, prevention, and treatment of skin and intestinal diseases, and in screening for therapeutic agents.
                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NM23; skin disease; intestinal disease; wound healing; vulnerary; ulcer; antitumour; gastrointestinal; dermatological; anti-inflammatory; tumour; antiulcer; nucleotide-diphosphate kinases; DNA-binding agent; psoriasis; transcription activating agent; Ras-GTPase regulator; Crohn's disease; NM23B; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel use of the NM23 protein family, for analysis, diagnosis, prevention and/or treatment of skin or intestinal diseases and/or wound healing and/or associated pathological
                                                                                                                                                                                                                                                                                                           1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                  1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                     100.0%; Score 803; DB 2; Length 152; 100.0%; Pred. No. 6.1e-90; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Regenbogen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWITCH BIOTECH AG.
ETH ZUERICH ETH ZENT HOENGGERBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goppelt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG80282 standard; protein; 152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 23; 48pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halle J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-FEB-2001; 2001EP-00103624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-FEB-2000; 2000DE-01008330.
24-APR-2000; 2000US-0199312P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Braun S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NM23B protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-490891/54.
                                                                                                                                                                                                                                                    Best Local Similarity
Matches 152; Conserv
                                                                                                                                                                                                      Sequence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP1127576-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2001
                                                                                                                                                                  lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ś
                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG80282;
                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (-LIMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ETHZ-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Werner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG80282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 888888888888888888
                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                             유
                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                            원
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
disturbances. The products of the invention have vulnerary, antitumour, gastrointestinal, dermatological, anti-inflammatory and antiuloer activity. The NM23 procein family act as nucleotide-diphosphate kinases, DNA-binding and transcription activating agents and regulators of Ras-GTPases. The proteins of the invention, antibodies (Ab) directed against them, and their encoding nucleic acids, or related vectors, transformed cells and antisense sequences, are used for analysis, diagnosis, prevention and/or treatment of skin and intestinal diseases (where associated with uncontrolled tissue growth or cell differentiation, particularly skin and intestinal tumours, also psoriasis, Crohn's disease and ulcers), wound healing and/or associated pathological alterations).

They are also used to screen for agents that are potentially useful for treating these conditions. In vitro monitoring of NM23 protein expression in tissue samples provides an early diagnosis of disease. This sequence in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human NM23 protein, useful for diagnosis and prognosis of cancer, and assessment of aggressiveness and susceptibility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKFGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                1 MANLERTFIAIKPDGVQRGLVGEIIKRPEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEBHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NM23-H1; NM23-H28; aggressiveness; metastatic potential; tumour; cancer susceptibility; early-onset familial breast cancer.
                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                             Length 152;
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                           100.0%; Score 803; DB 4;
100.0%; Pred. No. 6.1e-90;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USHE-) US DEPT SEC HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Col 19-20; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG79337 standard; protein; 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           King CR, Steeg PS, Liotta LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-00806932.
95US-00475684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00335948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                               tches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mature human NM23-H2S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-121137/16
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAI72922.
                                                                                                                                                                                                                                                                                                            Sequence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-DEC-1991;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L8-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6329198-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-DEC-2001
                                                                                                                                                                                                                                                                             invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG79337;
                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG79337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   $$$$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                                                                                                               ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

antibody and reagent

polynucleotides, polypeptides, antisense molecule, antibody and reagent are useful for preparing compositions for preventing, predicting or diagnosing, or a medicament for treating a cardiovascular disease, e.g. arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction. This sequence represents a protein identified in the invention a being differentially expressed in individuals with cardiovascular disease

ö

ö

; 0

0; Mismatches

Matches 152; Conservative

Local Similarity

Query Match

Sequence 152 AA;

888888888

Length 152 Indels

100.0%; Score 803; DB 6; 100.0%; Pred. No. 6.1e-90;

9 9

1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF

```
ö
                    H1 and H2S. These proteins are products of different genes, with NM23-H1 being localised to chromosome 17. These proteins are used to predict aggressiveness (metastatic potential) of human tumours and in genetic tests for cancer susceptibility, diagnosis and prognosis, also for selection of treatment, e.g. susceptibility to early-onset familial breast cancer. Gene nm23 may contribute to tumourigenicity and alteration in its regulation may be an early stage in the metastatic cascade. Allelic or homozygous deletion of the gene is detected in some primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a method of predicting, diagnosing or prognosing a cardiovascular disease by detection of a polymuclectide in a biological sample comprises hybridiaing at least one of the polymuclectide to a nucleic acid material of a biological sample, thus forming a hybridisation complex, and detecting the hybridisation complex. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PPGLVKYMNSGPVVAMVWEGLANVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.g.
detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
sequences given in AAG79335-38 show the related human proteins NM23-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cardiovascular disease, arteriosclerosis; ischaemia; angina pectoris; myocardial infarction; cardiant; antiarteriosclerotic; antianginal; gene therapy; differential gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Predicting, diagnosing or prognosing a cardiovascular disease, angina, ischemia, myocardial infarction or arteriosclerosis by of a polynuclectide in a biological sample comprises detecting hybridization complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein differentially expressed in cardiovascular disease #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 803; DB 5; 100.0%; Pred. No. 6.1e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schmitz G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 251-252; 454pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU89707 standard; protein; 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wick M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2002; 2002WO-EP011034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-OCT-2001; 2001GB-00024145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Munnes M, Gehrmann M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-403108/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ACA89880
                                                                                                                                                                                                                                                                                                                                                                 Sequence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003031650-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                   tumour cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU89707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU89107

IID ABU8

XX ABU8

DIT 10-J

XX ABU8

XX ABU8

XX ABU8

XX Gard

XX Gard

XX ABU8

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
```

```
The invention relates to a novel method for determining whether a test compound inhibits tyrosine kinase activity in a mammal comprising measuring in the mammal the level of at least one of the proteins and/or mRNA transcripts or genes for such proteins comprising type I plasminogen activator inhibitor (PAI-1), TIMP-1 (tissue inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining whether a test compound inhibits tyrosine kinase activity in a mammal by exposing the mammal to the test compound and measuring in the mammal the level of at least one of the measured proteins or mRNA
                                         FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                             tyrosine kinase activity; type 1 plasminogen activator inhibitor; PAI-1; TIMP-1; tissue inhibitor of metalloproteinase 1; vinculin; vascular endothelial growth factor; VEGF; placental growth factor; PLGF; migration inhibitory factor; MIG; human; nm23-H2.
1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O'farrell A, Smolich BD, Manning WC; Cherrington J;
                                                                                                     DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                     DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 90; 408pp; English.
                                                                                                                                                                                                           Ź
                                                                                                                                                                                                           ADH17091 standard; protein; 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAY-2002; 2002US-0380872P.
24-FEB-2003; 2003US-0448874P.
24-FEB-2003; 2003US-0448922P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAY-2003; 2003WO-US015711.
                                                                                                                                                                                                                                                                                                 Human nm23-H2 gene protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.
                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deprimo S
Schilling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-042604/04.
N-PSDB; ADH17090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SUGE-) SUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003097854-A2
                                                                                                                                                                                                                                                                    11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                        Ношо варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-FEB-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cranscripts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morimoto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Walter SA,
                                                                                                                                                                                                                                        ADH17091;
                                             61
                                                                                                      121
                                                                                                                                121
                                                                                                                                                                                             ADH17091
                                                                                                                                                                              RESULT
                                                                                                                                                                                                             셤
                                            ð
                                                                      음
                                                                                                   Š
                                                                                                                             요
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                           9
metalloproteinase 1), vinculin, vascular endothelial growth factor (VEGF), placental growth factor (PLGF), VEGF/PLGF heterodimers or migration inhibitory factor (MIG), exposing the mammal to the test compound and then measuring in the mammal the level of at least one of the proteins and/or mRNA transcripts previously measured. The method of the invention may be useful for determining whether a test compound inhibits tyrosine kinase activity in a mammal. The current sequence is that of the tyrosine kinase activity inhibition-related protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour-associated antigenic target, TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour-associated antigenic target (TAT) polypeptide PRO3637, SEQ:4888
                                                                                                                                                                                                                                                                                                                                                                                                     FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                      1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                            1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                             Score 803; DB 8; Length 152;
Pred. No. 6.1e-90;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; SEQ ID NO 4888; 7273pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABM81902 standard; protein; 152 AA
                                                                                                                                                                                                                               100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-SEP-2003; 2003WO-US028547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-OCT-2002; 2002US-0414971P.
                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu TD, Zhang Z, Zhou Y;
                                                                                                                                                                                                                                                                  Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prostate cancer or tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-347921/32.
N-PSDB; ACN40229.
                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                           Sequence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004030615-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-APR-2004
                                                                                                                                                          invention.
                                                                                                                                                                                                                                                                                                                                                                                  19
                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM81902;
                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM81902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8886888888888888
                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
```

```
coverent in carrier transfer to disposate and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acids an antibody specific for TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, anteagonists, binding molecules and compositions are useful antibodies, anteagonists, binding molecules and compositions are useful increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, carvical cancer, such as breast cancer, colorectal cancer, cervical cancer, inver cancers bladder cancer, cervical cancer, inver cancers, bladder cancer, cervical cancer, cancers of the central nervous system, melanoma and leukamia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in the inventors of the cancer and in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FPGLVKYMNSGPVVAMVWEGLAVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
and may thus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MANLERTFIAIXPDGVQRGLVGEIIXRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 803; DB 8;
100.0%; Pred. No. 6.1e-90;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                            represents a TAT polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Van Lookeren M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP23162 standard; protein; 152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO polypeptide SEQ ID NO:256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-OCT-2003; 2003WO-US034312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2002; 2002US-0423394P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clark H, Schoenfeld J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-419628/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADP23161
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004041170-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP23162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
ADP23162
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
```

```
(BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-FEB-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                      The invention relates to a novel isolated nuclear axid and the PRO coleopathic, antidatheric, anticheumatic, immunosuppressive, antidiflammatory, antidatheric, anticheumatic, immunosuppressive, costeopathic, antidatheric, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its antidatheric, hepatotropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, inventic chronic arthritis, a spondyloarthropathy, systemic selerosis, an idiopathic inflammatory myopathy, Sigern's syndrome, systemic sclerosis, autoimmune hemolytic anaemia, autoimmune therapy in the peripheral nervous disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Gulliain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, dulliain-Barre syndrome, confisease, infectious or autoimmune chronic active hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Mhipple's colisease, an autoimmune or immune-mediated skin disease, abullous skin disease, an autoimmune or immune-mediated skin disease, abullous skin disease, archne, allergic rhinitis, atopic dermatitis, poor an allergic rhinitis, atopic dermatitis, poor an allergic chronic phenomonia, idiopathic pulmonary fibrosis, graft rejection or contact dermatitis, dransplantation associated disease, graft rejection or graft-versus-host disease. The present sequence represents a PRO protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                             invention relates to a novel isolated nucleic acid and the PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyclin-dependent kinase modulation biomarker SEQ ID NO 205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; cyclin-dependent kinase; cdk; biomarker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 803; DB 8;
100.0%; Pred. No. 6.1e-90;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                SEQ ID NO 256; 2940pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADX05640 standard; protein; 152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUL-2004; 2004WO-US024424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-2003; 2003US-0490890P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2005012875-A2
      nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADX05640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
   {\tt F} \times {\tt W} \times {\tt OOCO} \\ {\tt O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
whether a mammal will respond or increase that control in the comprises measuring the level of one or more biomarkers selected from 2774 biomarkers given in the specification (nucleotide sequence SEQ ID NO:1246 (Genbank EST W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent modulating odk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed against the biomarkers and a cell culture model to identify biomarkers.

The cdk modulator is preferably N-5-[[5-(1,1-1)imethylethyl]-2-oxazolyy]methyllthol-2-thiazolyl-4-piperidine carboxamide, 0.5-Lutratic acid salt. Note: The sequence data for this patent did not form the printed specification, but was obtained in electronic format directly from WIDO at ftp. wipo.intt/pub/published_pct sequences. This sequence represents a biomarker used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCLQVGRNIHGS 120
                                                                                                                                                                              Biomarkers useful for predicting or determining the response of a mammal to a cancer treatment comprising administration of a modulator of cyclin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MANLERTFIAIKPOGVQRGLVGEIIKRFEQXGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic; Antithyrodd; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic; Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic; Antiallergic; ds; gene; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel method of predicting or determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
Wong TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 803; DB 9;
100.0%; Pred. No. 6.1e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
Jackson DG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                  Claim 5; SEQ ID NO 205; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADY14458 standard; protein; 152 AA
   Webster KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO polypeptide SEQ ID NO 264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                        to a cancer treatment comp
dependent kinase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 152; Conservative
                                                                    WPI; 2005-163068/17.
N-PSDB; ADX05639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
       Rupnow BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2005016962-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADY14458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
   Li M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADY14458
```

ö

```
for
human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of inhibitors of human-PRUNE cyclic nucleotide phosphodiesterase for preparation of medicament in the treatment of tumor metastases associated with overexpression of human-PRUNE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                        The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a PRO polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                         New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRN1IHGS
                                                                                                                                                                                                                                                                                                                                                                                                        1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a novel method for preparing a medicament the treatment of tumor metastases associated with overexpression of -PRUNE. The method comprise using inhibitors of human-PRUNE cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metastasis; therapeutic; gene expression; cytostatic; tumor; breast tumor; asrcoma; nervous system tumor; prostate tumor; pancreas tumor; colon tumor; rectal tumor; medulloblastoma; b-cell lymphoma; t-cell lymphoma; multiple myeloma; lung tumor;
                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor metastases treatment-related human PRUNE protein SeqID11
                                                                                                                                                                                                                                                                                                                             Length 152;
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                        100.0%; Score 803; DB 9;
100.0%; Pred. No. 6.1e-90;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                      Claim 8; SEQ ID NO 5499; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO 11; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEA89623 standard; protein; 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-DEC-2004; 2004WO-IT000689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-DEC-2003; 2003IT-RM000572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                  Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-445065/45.
WPI; 2005-182330/19
                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                     Sequence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2005056043-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZOLL/) ZOLLO M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-AUG-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEA89623
                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEA89623
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          엺
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09
                                                                                                                                                                                                                                                                                                                                                                  polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                        New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
Antiirheumatic; Antiarthitic; Osteopathic; Hemostatic; Antianemic;
Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                               invention relates to an isolated nucleic acid encoding a PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ď,
                                                                                                                                             Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 803; DB 9; Length 152; 100.0%; Pred. No. 6.1e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             쿭
                                                                                                                                             ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WI,
                                                                                                                                             MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood
                                                                                                                                             Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams MP,
                                                                                                                                             Williams MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID NO 264; 158pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADY19693 standard; protein; 152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRO polypeptide SEQ ID NO 5499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouyang W,
                                                                                                                                             Ouyang W,
                      11-AUG-2004; 2004WO-US026249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-AUG-2004; 2004WO-US026249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-AUG-2003; 2003US-0493546P
                                                              11-AUG-2003; 2003US-0493546P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antiallergic; diagnosis
                                                                                                      GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                   WPI; 2005-182330/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clark H,
                                                                                                                                             Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2005016962-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                             Abbas A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abbas A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
```

8 g ò ò 용

```
development of compounds with a cytostatic activity acting as human-PRUNE overexpression inhibitors. The invention is useful for preparation of medicaments in the treatment of tumor metastases, for example breast carcinoma, sarcoma, neuroblastoma, prostate tumor, pancreatic tumor, colonic tumor, rectal tumor, medulloblastoma, epitelioma, epatocarcinoma, cell T or cell B lymphomas, myeloma and melanoma and pulmonary tumor. As the h-PRUNE posses cyclic nucleotide phosphodissterase activity with preferential activity for camp over ceMP, the h-PRUNE overexpression can be effectively suppressed by certain PDE inhibitors thus the PDE inhibitors provides an effective alternative therapy for camp or the heavel of the development of the novel method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nm23 monoclonal antibody which recognizes human nm23 protein, useful for detecting tumors which have low levels of nm23 protein and thus an increased ability to metastasize or be malignant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 MANLERTFIAIKPDGVQRGLVGEIIKRPEQKGFRLVAMKFLRASEBHLKQHYIDLKDRPF 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
nucleotide phosphodiesterase. The invention may be useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; nm23-H2S; tumour metastasis; cancer susceptibility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "putative first amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 803; DB 9 100.0%; Pred. No. 7e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB14812 standard; protein; 176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-00475684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-00422801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-00806932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human nm23 protein nm23-H2S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steeg PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-531342/48.
N-PSDB; AAA70315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-1989;
11-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6087117-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liotta LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB14812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB14812
XX
AC AAB1
XX
AC AAB1
XX
AN Huma
XX
XX
AN Huma
XX
XX
AN Huma
XX
AN Huma
XX
AN Huma
XX
AN Huma
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             엄
```

Claim 1; Fig 6; 21pp; English

```
The invention relates to an isolated polynucleotide molecule encoding a human nm3 protein comprising nm23-HI having a sequence of 746 base pairs (bp) fully defined in the specification or nm23-H26 having a sequence of 670 bp fully defined in the specification. The polynucleotide molecule of the invention is useful as a diagnostic tool for detecting and/or determining RNA or DNA which can be employed to detect mRNA expression in cancer cells to aid in predicting the malignant potential of a human tumour. The DNA and the antibodies may also be used to detect
                                                                                                                                                                                                                                                 ö
The present sequence is the human nm23 protein nm23-H2S. Its coding sequence was isolated by searching a human lung cDNA library for sequences similar to pnm23-H2. Nm23 proteins are involved in tumour metastasis, and this protein, its gene and antibodies can be used to determine an individual's susceptibility to cancer and the likelihood of tumour metastasis within that individual. This is spossible using a number of methods, including Northern blotting, nuclease protection assays, in situ hybridisation, immunohistochemical analysis and solid phase
                                                                                                                                                                                                                                                                                                                                                   61 FPGLVKYMNSGPVVAMVWEGLAVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                         New DNA molecule encoding a human nm23 protein useful for predicting the malignant potential of a tumor and the genetic predisposition for developing cancer, comprises nm23-H1 and nm23-H2s genes.
                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                      25 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGPRLVAMKFLRASEEHLKQHYIDLKDRPP
                                                                                                                                                                                                                                                                                   1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASBEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human nm23 protein; nm23-H1; nm23-H2S; cancer; malignant potential;
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                Length 176;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                          100.0%; Score 803; DB 3;
100.0%; Pred. No. 7.6e-90;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human tumour; genetic predisposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA026423 standard; protein; 176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 6; 21pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein of the nm23-H2S cDNA.
                                                                                                                                                                                                                              Best Local Similarity 100.0%;
Matches 152; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-00806932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89US-00422801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-705184/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                King CR, Steeg PS,
                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAL53615.
                                                                                                                                                                                 Sequence 176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6423836-B1
                                                                                                                                                  immunoassays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA026423;
                                                                                                                                                                                                                                                                                                                                                                                             85
                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA026423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8888888888888
                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                            유
                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

œ

```
Allelic or homozygous deletion of the gene is detected in some primary
                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-2004; 2004US-00013684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-DEC-2003; 2003TW-00136309.
                                                                                                                                                                                                                                                                                                                                            25-AUG-2005 (first entry)
                                                                                       Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-444137/45
                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seng T, Cheng P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 151 AA;
                                            Sequence 176 AA
                      tumour cells
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-2005.
                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                     AEA90109;
                                                                   Query Match
                                                                              Local
                                                                                                                                                                                                                                                                       RESULT 15
AEA90109
                                                                                                                                                                                                                                                                                                          Š
         ន្តដ្ឋប្ល
                                                                                                                                      셤
                                                                                                                                                                                   셤
                                                                                                                                                               ð
                                                                                                                                                                                                             ŝ
                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAG79335-38 show the related human proteins NM23-H1 and H2S. These proteins are products of different genes, with NW23-H1 being localised to chromosome 17. These proteins are used to predict aggressiveness (metastatic potential) of human tumours and in genetic tests for cancer susceptibility, diagnosis and prognosis, also for tests for cancer. Seatment, e.g. susceptibility to early-onset familial breast cancer. Gene nm23 may contribute to tumourigenicity and alteration in its regulation may be an early stage in the metastatic cascade.
genetic predisposition for developing cancer. The human mm23 protein can be employed to produce nm23 antibodies. This sequence represents the nm23-H2S protein of the invention
                                                                                                                                                                                     61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                  85 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer, and
                                                                                                                                        9
                                                                                                                                                               84
                                                                                                                                        1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                    25 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  NM23-H1; NM23-H2S; aggressiveness; metastatic potential; tumour; cancer susceptibility; early-onset familial breast cancer.
                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human NM23 protein, useful for diagnosis and prognosis of assessment of aggressiveness and susceptibility.
                                                                                        100.0%; Score 803; DB 5; Length 176; 100.0%; Pred. No. 7.6e-90;
                                                                                                                 Indels
                                                                                                                  ;
0
                                                                                                                                                                                                                                    121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                   Human NM23-H2S encoded from full length cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US DEPT SEC HEALTH & HUMAN SERVICES.
                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25. .176
/label= Mature NM23-H2S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    AAG79336 standard; protein; 176 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Col 19-22; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liotta LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89US-00422801.
91US-00806932.
95US-00475684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00335948
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                    Best Local Similarity 100.
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-121137/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steeg PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAI72992
                                                                   Sequence 176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6329198-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                    21-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-DEC-2001
                                                                                                                                                                                                                                                                                                                                             AAG79336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    King CR,
                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USHE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                              RESULT 14
         8
                                                                                                                                                                                                            g
                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                       ઠે
```

```
ö
                                                                ö
                                                                                                                                                                                                                                                                                                               144
                                                                                                                             9
                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention also relates to the use of an autoantigen screening method to identify biomarkers that can be used in detecting liver diseases such as liver cirrhosia and liver cancer. The present sequence is the human nucleoside diphosphate kinase protein. This sequence is the autoantigen identified from cell lines using sera of patients with liver cirrhosis
                                                                                                                                                                                                                                                                                     2 ANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFF
                                                                                                                       1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                        61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIOVGRNIIHGS
                                                                                                                                                                                        25 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Selectable marker; screening; diagnosis; liver disease; hepatotropic; gastrointestinal disease; liver cirrhosis; liver cancer; cytostatic; neoplasm; antigen; nucleoside diphosphate kinase; enzyme.
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New biomarker for liver diseases comprising specific sequences, use for developing kits for diagnosing liver cirrhosis or liver cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel biomarkers for liver diseases. The
                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
   Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 99.4%; Score 798; DB 9; Length 151; Best Local Similarity 100.0%; Pred. No. 2.5e-89; Matches 151; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human nucleoside diphosphate kinase protein, SEQ ID NO: 1.
                                                             Indels
                                                                ö
Score 803; DB 5;
Pred. No. 7.6e-90;
                                                                                                                                                                                                                                                                                                                                                                                                             145 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 176
                                ; Pred. No. 7.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INTE-) IND TECHNOLOGY RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEA90109 standard; protein; 151
```

```
Db 1 ANLERTFIAİKPDGVQRGLVGELIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFF 60

Qy 62 PGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCLQVGRNIHGSD 121
```

		61 PGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSD 120
		-
		ß
!	=	Ä
į	_	Ξ
:	_	S
;	=	5
,	=	8
	=	Ĕ
	_	Ĕ
	=	ᅜ
i	=	H
•	=	Ħ
	=	ĕ
;	=	SK
1	=	8
:	_	<u> </u>
	=	É
;	_	8
Ì	_	ě
:	_	٤
i	=	8
;	=	Đ.
:	_	5
	=	Ę
;	=	뎚
į	_	ĕ
:	=	Ž
	=	₹
	_	3
4	_	ď.
Ś	=	S
1	=	₹
į	=	8
:	_	ξ
j	=	g
•	_	Д
9		Ξ.
•		Ψ

a & a

Search completed: December 16, 2005, 16:43:39 Job time: 127.667 secs

This Page Blank (uspic)

```
December 16, 2005, 16:39:14; Search time 7.30818 Seconds (without alignments) 153.021 Million cell updates/sec
                                                                                                                                                                                                                                                                             US-10-074-694-3
876
1 QSQPAVKPCHLKGTMANSER......WFQPBELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA New:*

1: /cgn2 6/ptodata/1/pubpāa/USO9 NEW PUB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/USO8 NEW_PUB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/PUSIW PUB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/PUSI NEW PUB.pep:*

7: /cgn2 6/ptodata/1/pubpaa/USI NEW_PUB.pep:*

7: /cgn2 6/ptodata/1/pubpaa/USI NEW_PUB.pep:*

8: /cgn2 6/ptodata/1/pubpaa/USI NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51470
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51470 seqs, 6736768 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                                     Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

•		d			SUMMARIES	
Result No.	Score	Query Match	å Query Match Length	DB	ID	Description
-	759	86.6	152	9	US-10-878-556A-49	Seguence 49, Ap
8	729	83.2	152	9	10-821-	157
e	333.5	38.1	136	7	US-11-055-822-966	
4	333.5	38.1	136	7	US-11-055-822-994	
ស	303	34.6	141	9	US-10-467-657-4110	
9	7	8.7	428	9	US-10-763-712A-118	Sequence 118, P
7	73.5	8.4	1144	9	US-10-467-657-1820	
8	69.5	7.9	1302	7	US-11-090-439-42	4
σ	69	7.9	795	9	US-10-770-726-49	
10	68	7.8	293	9	2	Sequence 4834,
11	67	7.6	2261	9	US-10-995-561-600	
12	66.5	7.6	364	9	US-10-131-826A-342	
13	66.5	7.6	364	7	US-11-091-334-2	
14	99	7.5	428	9	US-10-793-626-2050	8
15	64	7.3	1101	9	œ	
16	63.5	7.2	295	7	US-11-143-980-31	
17	63.5	7.2	347	9	US-10-467-657-6092	609
18	63.5	7.2	347	9	US-10-467-657-7548	
19	63	7.2	366	9	US-10-510-386-42	4
20	62.5	7.1	299	7	US-11-055-822-408	Sequence 408, 7
21	62.5	7.1	365	7	ᇽ	6
22	62.5	7.1	365	7	US-11-080-991-78	2
23	62	7.1	375	7	US-11-051-267-16	ĭ
24	62	7.1	527	9	US-10-821-234-1574	ä
25	61.5	7.0	480	9	US-10-510-386-12	Sequence 12, Ap

Sequence 2758, Ap Sequence 6728, Ap Sequence 6728, App Sequence 22, Appl Sequence 12, App Sequence 161, App Sequence 119, App Sequence 117, App Sequence 270, App Sequence 270, App Sequence 34, Appl Sequence 354, App Sequence 15, Appl Sequence 11, Appl Sequence 15, Appl Sequence 11, Appl Sequence 12, Appl Sequence 12, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 27, Appl	on Length 152; Indels 0; Gaps 0; FLQASEDLLKEHYTDLKDRPF 74	MGASEDLIKEHITTIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
US-10-467-657-2758 US-10-467-657-6728 US-10-763-712A-18 US-10-763-712A-99 US-11-069-642-22 US-10-467-657-764 US-10-467-657-764 US-10-129-143-179 US-10-793-626-266 US-10-793-626-266 US-10-793-626-266 US-10-793-626-266 US-10-793-626-270 US-10-783-626-270 US-10-67-59-68 US-10-67-59-68 US-10-67-295-71 US-10-67-295-71 US-10-67-295-71 US-10-67-712A-15 US-11-074-176-142	GNMENTS otein expressi 8,556A dka_human 759, DB 6; No. 3.3e-72; smatches 6; KRFGGGRLVGLK KRFGGGGRLVGLK	MANCERTEIAININININININININININININININININININI
7.0 618 7.0 1206 6 7.0 1206 6 7.0 1206 6 7.0 610 7 7.0 610 7 7.0 610 7 6.9 459 6 6.9 459 6 6.8 346 1 6.8 1061 6 6.8 201 6 6.8 451 6	ALIL SULT 1 10-878-556A-49 Sequence 49, Application US/10878556A Publication No. US20050266399A1 GENERAL INFORMATION: APPLICANT: Hoffmann La-Roche Inc. TITLE OF INVENTION: HCV regulated pr. FILE REFERENCE: 21762 CURRENT APPLICATION NUMBER: US/10/87 CURRENT PILING DATE: 2004-06-28 NUMBER OF SEQ ID NOS: 199 SOFTWARE: PATENT OF SEQ ID NOS: 199 LENGTH: 152 TYPE: PRT ORGANISM: HOMO Sapiens PUBLICATION INFORMATION: DATABASE ACCESSION NUMBER: sw hum/n DATABASE ENTRY DATE: 1990-04-01 -10-878-556A-49 QUELY MATCH Beet Local Similarity 94.1%; Pred. Matches 143; Conservative 3; Mi matches 143; CONSERTEIAKPDGVORGIVEEII	Db 1
26 61.5 27 61.5 29 61.5 30 61.5 31 61.5 32 61.5 33 60.5 34 60.5 34 60.5 36 60.5 37 60.5 39 60.5 39 60.5 44 59.5 45 59.5 45 59.5	RESULT 1 US-10-878-556A-49 Sequence 49, Applica Publication No. US20 GENERAL INFORMATION: TITLE OF INVENTION: FILE REFERENCE: 27 CURRENT APPLICATION CURRENT FILING DATE NUMBER OF SEQ ID NO SOFTWARE: PATENTION: SEQ ID NO 49 LENGTH: 152 TYPE: PRT ORGANISM: HOME SAP PRELICATION INFORMAP PUBLICATION INFORMAP US-10-878-556A-49 QUETY MATCH BEST LOCAL SIMILATIC BEST LOCAL SIMILATIC MATCHES 143; CORSE	Db 1

```
Query Match
Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-055-822-994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                     유
                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PPGLVKYMNSGPVVAMVWEGLMVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 966
LENGTH: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pompejus, Markus
APPLICANT: Rroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Calder, Oskar
APPLICANT: Calder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: ONWHER: US/11/055,822
CURRENT FILING DATE: 2006-06-23
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1999-07-08
PRIOR PRILING DATE: 1999-07-08
PRIOR PRILING DATE: 1999-07-08
PRIOR PRILING DATE: 1999-07-08
PRIOR PRILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                               Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                      Score 729; DB 6; Li
Pred. No. 4.3e-69;
9; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                    CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Corynebacterium glutamicum
US-11-055-822-966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 966, Application US/11055822
Publication No. US20050260707A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.1%;
Matches 137; Conservative
                                                                                                                                                                                                                                                     TYPE: PRT

ORGANISM: Homo sapiens
US-10-821-234-1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

```
78 LVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNP-ADSKPGTIRGDFCIQVGRNIIHGSDS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                          62 LVEFITSAPLIAGIVEGERAIDAWRQLAGGTDPVAKATPGTIRGDFALTVGENVVHGSDS 121
                                                                                                                                                                                                                                                                                                               78 LVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNP-ADSKPGTIRGDFCIQVGRNIIHGSDS 136
                                                                                                                                                             18 SERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPFFTG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 SERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPFFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TERTLILIKPDGVTNGHVGELIARIERKGLKLAALDLRVADRETAEKHYEEHADKPFFGE
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Aroger, burkhard
APPLICANT: Calcaer, burkhard
APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Oskar
APPLICANT: Zelder, Oskar
APPLICANT: Aberhauer, Gregor
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
TITLE OF INVENTION NUMBER: US/11/055,822
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-00-06-25
PRIOR FILING DATE: 1999-00-06
PRIOR FILING DATE: 1999-00-07
PRIOR FILING DATE: 1999-00-07
PRIOR FILING DATE: 1999-00-01
PRIOR FILING DATE: 1999-00-08
PRIOR FILING DATE: 1999-00-09
38.1%; Score 333.5; DB 7; Length 136; 49.2%; Pred. No. 4.9e-28; ive 24; Mismatches 42; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 38.1%; Score 333.5; DB 7
Best Local Similarity 49.2%; Pred. No. 4.9e-28;
Matches 65; Conservative 24; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 994, Application US/11055822
Publication No. US20050260707A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 VKSAEKEISLWF 148
                                                                                  65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||:|||:||
122 PESAEREISIWF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 VKSAEKEISLWF 148
```

9

셤

```
68 ------DLKDRPFFTGLV----KYMHSGPVVAMVWEGLNVVKTGRVMLG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AGIKPVGAADVWIGNPNAPDKPFRAMLVIRNDAGYLRLSELLTEAYVG----QDRNIHHA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 GLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDS 136
                                                                                                                                                                                    ---FANNLAQALEI 314
                                               21 TFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEH----YTDLKDRPFFT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 SERTFIAIK-----PDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 ETNPADSKPGTIRGDFCI-----QVGRNIIHGS-DSVKSAEKEISLWFQPE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-090-439-42

US-11-090-439-42

Sequence 42, Application US/11090439

Publication No. US20050266442A1

GENERAL INFORMATION:

APPLICANT: Squillace, Rachel

APPLICANT: Weiner, Michael P.

TITLE OF INVENTION: Amglomyolipoma Cell and Method of Use Thereof

FILE REFERENCE: 2418-502

CURRENT APPLICATION NUMBER: US/11/090,439

CURRENT FILING DATE: 2005-03-25

PRIOR APPLICATION NUMBER: 60/556,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 1144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59; Indels
61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PONTANA Mariagrazia
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
                                                                                                                                                                      271 GAISRVINNADL-LYGKAKELYEANKDLLKGTNP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 19.5%; Pred. No. 7.9;
Matches 37; Conservative 39; Mismatches
26; Mismatches
                                                                                                                                                                                                                                                                      315 VYFIERAIDLLDEALAKWPIKPRDEVEIK 343
                                                                                                                                                                                                                                      137 VKSAEKEISL-----W-FOPEELVEYK 157
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1820, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SegWin99, version 1.04
SEQ ID NO 1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Neisseria gonorrhoeae US-10-467-657-1820
  32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | |:::|
175 LPERPEWEAC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 --ELVEYKSC 159
                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-10-467-657-1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                           원
                                                                                                                                          ò
                                                                                                                                                                                       ದ್ದ
                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dillon, Harrison F.
TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
TITLE OF INVENTION: Production
FILE REFERENCE: H2042101-CTP
CURRENT FILING DATE: 2004-01-21
FRICH FILING DATE: 2004-01-21
PRIOR FILING DATE: 2002-11-04
PRIOR FILING DATE: 2003-04-12
PRIOR FILING DATE: 2003-04-12
PRIOR FILING DATE: 2003-04-12
PRIOR FILING DATE: 2003-09-03
NUMBER OF SEQ ID NOS: 184
SOFTWARE: Patentin version 3.2
SEQ ID NO 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 VKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVK 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 VEFMTGGPVMIQVLEGENAVLKNRELMGATNPTEAAEGTIRADFATSVSINAVHGSDSVE 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ERTISIIKPDAVGKAVIGKIYSRPEENGLKIVAAKMKQLTLKEAQEFYAVHKDRPFYAGL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 ERTFIAIKPDGVORGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPFFTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch
1 Similarity 44.4%; Pred. No. 7.5e-25;
60; Conservative 23; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 428;
                                                                                                                                                                                                                                                          APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MANACI Elisabetta
APPLICANT: MONACI Elisabetta
TILLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 76; DB (
Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
FRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 4110
LENGTH: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 118, Application US/10763712A Publication No. US20050266541A1 GENERAL INFORMATION:
APPLICANT: Solazyme, Inc.
                                                                                                                      US-10-467-657-4110
; Sequence 4110, Application US/10467657
; Publication No. US20050260581A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.7%;
21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 SAEKEISLWFQPEEL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 NAALEIAYFFSQTEI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pyrococcus furiosus
                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
  :|||:|||:||
122 PESAEREISIWF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-10-763-712A-118
```

TYPE: PRT

셤

요 ò

ઠે

9

```
US-10-995-561-600

J Sequence 600, Application US/10995561

Sequence 600, Application US/2054A1

Sequence 600, Application Wo. US20050272054A1

GENERAL INFORMATION:

TITLE OF INVERVION:

CURRENT APPLICATION UNDERS:

CURRENT PILIABING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FASESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 EDLLKEH-----YIDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNP-- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 --LLKERPEKFIVFCD--DLSFESGDETY----KALKTALDGGLSQRCANVMVYATSNRR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 -----ADSKPGT--IRGDFCIQVGRNIIHGSDSVK---SAEKEISLW--FQPEELVEYK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 HLMPEYLDENAGTTGVRGE-----IHOKEAVEEKVSLSDRFGLWLSFYPFDQNDYL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 NSERTFIAIKP-----DGV----QRGLVGEIIKRFEQKGFR------LVGLKFLQAS
                                                                                                                                                                                                                                                                                                                                                                                                                         58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 EHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : | : | : | | : | | : | | : | 344 ETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPA 391
/ Match 7.6%; Score 67; DB 6; Length 2261; Local Similarity 25.0%; Pred. No. 90; as 12; Conservative 12; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.8%; Score 68; DB 6; Length 293; Best Local Similarity 24.1%; Pred. No. 5.1; Matches 45; Conservative 27; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-131-826A-342
; Sequence 342, Application US/10131826A
; Publication No. US20050245730A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCAONWI 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 AAVRSWL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-995-561-600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
TITLE REFERENCE: AMA101079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 486400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 PALSPIELKQELPKYLPALQGCRSVEEFQCL--NRIEEGTYGVVYRAKDKKTDEIVALKR 468
                                                                                                                                                                                                                                                                                                                                              84 SGPVVAMVWEGLNV---VKTGRVMLGE--TNPADSKPG-TIRGDFCI---QVGRNIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 LQASEDLLKEHY--TDLKDRPFFTGLVKYMHSGPVVAMVWE---GLNVVKTGRVM----- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 PAVKPCHLKGTM-----ANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKF 54
                                                                                                                                                                                                                                                             36 GEIIK-RFEOKGFR-----LVGLKFLQASEDLLKEHYTDLKDRPFFTGLVKYMH- 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72; Gaps
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                              / Match 7.9%; Score 69.5; DB 7; Length 1302; Local Similarity 23.7%; Pred. No. 24; nes 36; Conservative 29; Mismatches 58; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.9%; Score 69; DB 6; Length 795; Best Local Similarity 20.7%; Pred. No. 15; Matches 46; Conservative 31; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 -----EYKSCAQNW 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        867 EAIYGFEESCSIWYPNKQVQRRLWLEYEDISK 898
                                                                                                                                                                                                                                                                                                                                                                                                                           135 DSVKSAEKEISLWFQPEEL-----VEYKSCAQ 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 ----LGETNPADSKPGTIRGDFCIQVGRNIH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4834, Application US/10467657 Publication No. US20050260581A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49, Application US/10770726 Publication No. US20050266409A1 GENERAL INFORMATION:
                NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 42
LENGTH: 1302
TYPE: PRT
ORGANISM: Homo sapiens
US-11-090-439-42
  PRIOR FILING DATE: 2004-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-10-467-657-4834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-770-726-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-770-726-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 49
LENGTH: 795
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
```

ö

```
US-10-793-626-2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-091-334-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C128
CURRENT PILIDR DATE: 2002-04-24
FRICH APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/049911
PRIOR APPLICATION NUMBER: 60/059118
PRIOR APPLICATION NUMBER: 60/059118
PRIOR APPLICATION NUMBER: 60/059118
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 SQASSCLQKLLYFNLSAIKEREQLTLAQLGLDLGPNSYYNLGPELEL---ALFLVQEPHV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 LQASEDLLKEHYTDL---KDRPFFT-----GLVKYMHSGPVVAMVWEGLNVVKTGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 MLGETNPADSKPGTIRGDFCIQVGRNIIH-----GSDSVKSAEKEISLW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 OPAVKPCHLKGTMANSERTFIAIKPDGVQR-----GLVGEIIKRFEQKGFRLVGLKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 550 SEQ ID NO 342 LENGTH: 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.6%; Score 66.5; DB 6; Length 364; Best Local Similarity 24.2%; Pred. No. 9.7; Matches 48; Conservative 23; Mismatches 70; Indels 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----FOPEELVEYKSCAQ 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stewart, Timothy A
                                                                            Gao,Wei-Qiang
Gerritsen,Mary E.
                                                                                                                                                                                                                                                                                                         Watanabe, Colin K
Wood, William
                                                                                                                                                       Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                            Sherwood, Steven
                                                                                                                            Goddard, Audrey
                                                                                                                                                                                                                                 Smith, Victoria
DeForge, Laura
                                                                                                                                                                                                                                                                                 Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-10-131-826A-342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

RESULT

```
55 LQASEDLLKEHYTDL---KDRPFFT-----GLVKYMHSGPVVAMVWEGLNVVKTGRV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 SQASSCLQKLLYFNLSAIKEREQLTLAQLGLDLGPNSYYNLGPELEL---ALFLVQEPHV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 MLGETNPADSKPGTIRGDFCIOVGRNIIH-----GSDSVKSAEKEISLW----- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 W-GQİTPKREKMEVLKS---VPWPQGAVHFNLLDVAKDWNDNPRKNFGLFLEILVKEDRD 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2050, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERAY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PUJ480US
CURRENT FILING DATE: 204-03-04
PRIOR PELING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 QPAVKPCHLKGTMANSERTFIAIKPDGVQR-----GLVGEIIKRFEQKGFRLVGLKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.6%; Score 66.5; DB 7; Length 364;
24.2%; Pred. No. 9.7;
tive 23; Mismatches 70; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 66; DB 6; Length 428;
Pred. No. 14;
GRUEGE 13.34.

GRUEGEL INCORPATION US/11091334

GRUEGAL INFORMATION:

APPLICANT: SOPPEC, et al.

TITLE OF INVENTION: Growth Factor HTTER36

FILE REFREENCE: PP230P1

CURRENT APPLICATION NUMBER: US/11/091,334

CURRENT FILING DATE: 2005-03-29

PRIOR FILING DATE: 2005-03-30

PRIOR PRIOR DATE: 2002-04-08

PRIOR PILING DATE: 2002-04-08

PRIOR PILING DATE: 1999-07-21

SROID PILOR PILING DATE: 1999-07-21

SROID PRIOR PILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PATEURING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 ----FQPEELVEYKSCAQ 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 SGVNFQPED----TCAR 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 24.2
Matches 48, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
```

```
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                           163 ------FTHKKPLPKFLTL----FAGPLFNFILALVLFIGLAYYQGTPTNVIGEVV- 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 GLKFLQASEDLLKEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGL---NVVKTGRVMLGE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 TNPAD------SKPGTIRGDFCIQVGRNIIHGSDSVKSAEKEIS-----LWFQ 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 ASEDLLKEHYTDLKDRPFFTGLVKYMHSGP----VVAMV-----WEGLNVVKTGRVML 105
                                     6 VKPCHLKG-----TMANSERTF--IAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LVGEIIKRFEQK-GFRLV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Gaps
 48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.3%; Score 64; DB 6; Length 1101; Best Local Similarity 22.6%; Pred. No. 73; Matches 43; Conservative 26; Mismatches 83; Indels
39; Conservative 19; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                      Sequence 107, Application US/10878556A
Publication No. US20050266399A1
GENERAL INFORMATION:
APPLICANT: HOFfmann La-Roche Inc.
TITLE OF INVENTION: HCV regulated protein expression
FILE REFERENCE: 21762
CURRENT APPLICATION NUMBER: US/10/878,556A
CURRENT FILING DATE: 2004-06-28
NUMBER OF SEQ ID NOS: 199
SOFTWARE: PatentIn version 3.1
IENGTH: 1101
                                                                                                                                                                                          106 GETNPADSKPGTIRGDFCIQVGRNIJHGSDSVK 138
                                                                                                                                                                                                              209 - KKSPAD-EAGLHKGDKIVQVGNHKIKNFDDIK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: sw hum/acly_human
DATABASE ENTRY DATE: 1996-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 OSOPAVKPCHLKGTMANSERTFIAIKPDGVQRG-
                                                                                                                                                                                                                                                                                        RESULT 15
US-10-878-556A-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-878-556A-107
 Matches
                                                                     셤
                                                                                                                 ઠે
                                                                                                                                           g
                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
```

Search completed: December 16, 2005, 17:01:57 Job time : 8.30818 secs

150 PEELVEYKSC 159 : | : | | | 880 -KRLPKY-SC 887

S G

```
Sequence 2, Application US/09791118A

Patent No. US20020034741A1

GENERAL INFORMATION

APPLICANT: Merner, Sabine

APPLICANT: Penzberg, Jorn-Peter

APPLICANT: Regenbogen, Johannes

TITLE OF INVENTION: encoding these of the gene family NM23 for the diagnosis or

TITLE OF INVENTION: treatment of skin or intestinal disorders, and their use for

TITLE OF INVENTION: the identification of pharmacologically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-10-732-923-13110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-732-923-13110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-09-791-118A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13110, A Sequence 2, Appli Sequence 13111, A Sequence 1314, A Sequence 426, Appli Sequence 13, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11, Appl
110, App
13341, A
13355, A
2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13353, A
21, Appl
13354, A
3, Appli
                                                                                                                                                      December 16, 2005, 16:38:19 ; Search time 117.453 Seconds (without alignments) 590.532 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                  1 QSQPAVKPCHLKGTMANSER........WFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-732-923-13110
US-10-732-923-13111
US-10-732-923-13111
US-10-732-923-13111
US-10-732-923-13111
US-10-732-923-13140
US-11-013-684-2
US-11-013-684-2
US-11-013-684-2
US-11-013-684-2
US-10-732-923-13126
US-10-732-923-13342
US-10-732-923-1335-100-133-628-1
US-10-732-923-1335-100-133-628-1
US-10-732-923-1335-100-133-628-1
US-10-732-923-1335-100-133-628-1
US-10-732-923-1335-100-132-923-1335-100-133-628-1
US-10-732-923-1335-100-133-628-2
US-10-732-923-1335-100-133-628-2
US-10-732-923-1335-100-133-628-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-732-923-13132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-791-118A-3
US-10-232-188-5
US-10-133-628-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA Main:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1867569 segs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                      US-10-074-694-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               774.5
774.5
774.5
759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                         OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
```

Š

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLKEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LIKEHYTDLKDRPFFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRG 120
                                                                 13127, A
332, Appl
3313, App
13113, A
13320, A
13336, A
13334, A
13317, A
13117, A
90, Appl
13345, A
352, App
13346, A
1, Appli
4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13336, 1
Sequence 13134, 1
Sequence 13117, 1
Sequence 13315, 1
Sequence 13119, 1
                                                                                        332, Ap
13113,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QSQPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                            Sequence 13110, Application US/10732923

Publication No. US20050108791A1

GENERAL INFORMATION:

APPLICANT: Edgerton. Michael D

TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES

FILE REFERENCE: 38-15(52796)C

CURRENT APPLICATION NUMBER: US/10/732,923

CURRENT FILING DATE: 2003-12-10

PRIOR FILING DATE: 2003-12-04

NUMBER OF SEQ ID NOS: 24149

SEQ ID NO 13110
                                                                 Sequence
Sequence
Sequence
                                                                                                           Sequence
Sequence
Sequence
            Sequence
Sequence
                                                                                                   Sequence
                                             Sequence
                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFCIQVGRNIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
US-10-440-464-90

US-10-732-923-13345

US-10-563-929-352

US-10-732-923-13346

US-10-133-628-4

US-10-133-628-4

US-10-732-923-13127

US-10-722-923-13120

US-10-732-923-13128

US-10-732-923-13128

US-10-732-923-13128

US-10-732-923-13128

US-10-732-923-13128

US-10-732-923-13134

US-10-732-923-13134

US-10-732-923-13117

US-10-732-923-13117

US-10-732-923-13117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 876; DB 5;
100.0%; Pred. No. 3.3e-88;
cive 0; Mismatches 0;
                                                                                                                                                                                                                            ALIGNMENTS
  1522
1523
1523
1523
1523
1523
1523
1523
  83.2
883.2
882.6
882.6
882.6
882.6
81.1
11.2
811.3
811.3
```

N

```
SEQ ID NO 13112
LENGTH: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-09-833-790-426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 FIGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FIGLVKYMHSGPVVAMVWEGLNVVKTGRVWLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 MANSERTFIAIKPDGVORGLVGBIIKRFEOKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13111, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
    APPLICANT Edgerton, Michael D
    TITLE OF INVENTION: TANSGEBIC PLANTS WITH IMPROVED PHENOTYPES
    CURRENT APPLICATION NUMBER: US/10/732,923
    CURRENT FILING DATE: 2003-12-10
    PRIOR APPLICATION NUMBER: 10/310,154
    NUMBER OF SEQ ID NOS: 24149
    SEQ ID NO 13111
    LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 152;
                                                                                                                                                                                                                                                                                                                                                                 Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 91.1%; Score 798; DB 5; I
Best Local Similarity 100.0%; Pred. No. 1.2e-79;
Matches 152; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                               Query Match 91.1%; Score 798; DB 3; I
Best Local Similarity 100.0%; Pred. No. 1.2e-79;
Matches 152; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 DSVKSAEKEISLWFOPEELVEYKSCAONWIYE 152
                FILE REFERENCE: 50125/012002
CURRENT APPLICATION NUMBER: US/09/791,118A
CURRENT FILING DATE: 2001-02-22
FRIOR APPLICATION NUMBER: US 60/199,312
FRIOR FILING DATE: 2000-04-24
FRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 152
TITLE OF INVENTION: active substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus US-10-732-923-13111
                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-732-923-13111
                                                                                                                                                                                                                                                                                                                   US-09-791-118A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

US-10-732-923-13112 ; Sequence 13112, Application US/10732923 ; Publication No. US20050108791A1

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 KEHYVDLKDRPFFAGLVKYMHSGPVVAMVWEGLAVVKTGRVWLGETNPADSKPGTIRGDF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 QPEFKPKQLEGTMANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 QPEFKPKQLEGTMANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 OPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 QPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 426, Application US/09833790

Fatent No. US20020068288A1

GENERAL INFORMATION:

APPLICANT: Lodes, Michael J.

APPLICANT: Secrist, Heather

APPLICANT: Mohamath, Raddoh

APPLICANT: Mohamath, Raddoh

APPLICANT: Fan, Ligun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.512

CURRENT APPLICATION NUMBER: US/09/833,790

CURRENT PILING DATE: 2001-04-11

NUMBER OF SEQ ID NOS: 4400

SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE 38-15(52796) C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR PEDFLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 794; DB 3; Length 178;
Pred. No. 4.1e-79;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                     Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 CIQVGRNIIHGSDSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                      10; Indels
                                                                                                                                                                                                                                                                                                                                                  Score 794; DB 5;
Pred. No. 4.1e-79;
4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.5%;
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 91.5%;
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-833-790-426
                                                                                                                                                                                                                                                                             ; ORGANISM: Mus musculus
US-10-732-923-13112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
Sequence 42, Application US/11037713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-10-732-923-13126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 KEHYVDLKDRPFFAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 KEHYVDLKDRPFFAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 OPBFKPKOLEGIWANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 OPAVKPCHLKGTWANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 OPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                US-10-732-923-13340
; Sequence 1340, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE COF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(2796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT PILING DATE: 2003-12-10
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13340
; LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 794; DB 6; Length 180;
Pred. No. 4.2e-79;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                               Query Match 90.6%; Score 794; DB 5; Length 180; Best Local Similarity 91.5%; Pred. No. 4.2e-79; Matches 150; Conservative 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 CIOVGRNIIHGSDSVESAEKEIGLWFHPEELVDYTSCAONWIYE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIQVGRNIIHGSDSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 CIQVGRNIIHGSDSVKSABKEISLWFQPEELVBYKSCAQNWIYB 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 90.6%;
Best Local Similarity 91.5%;
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-732-923-13340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CRGANISM: Human
US-11-013-684-2
                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
```

```
61 FSGLVKYMASGPVVAMVWEGLAVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 QPEFKPKQLEGTWANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFWQASEDLL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFIQASEDLLKEHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 QPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13126, Application US/10732923
; Sequence 13126, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15 (2796) C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR PILING DATE: 2003-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1126
                                                                                   APPLICANT: BERUCCI, FRANCOIS
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: DEBONO, STEPHANE
APPLICANT: TAGENO, STEPHANE
TITLE OF INVENTION: PROTEIN EXPRESSION PROFILLING AND BREAST CANCER
TITLE OF INVENTION: PROCENOSIS
FILE REPERRENCE: 1016-R-04(B)
CURRENT APPLICATION NUMBER: US/11/037,713
CURRENT PILING DATE: 2005-01-18
PRIOR APPLICATION NUMBER: 60/537,412
PRIOR PILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VOY: 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 90.6%; Score 794; DB 6; Length 180; Best Local Similarity 91.5%; Pred. No. 4.2e-79; Matches 150; Conservative 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 CIQVGRNIIHGSDSVESAEKEIGLWFHPBELVDYTSCAQNWIYE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 779; DB 5;
Pred. No. 1.5e-77;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 96.7%;
Matches 147; Conservative
Publication No. US20050221398A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT

ORGANISM: Rattus norvegicus
US-10-732-923-13126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRGANISM: Homo sapiens US-11-037-713-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135
```

ö

RESULT 8 US-11-037-713-42

```
Sequence 19, Application US/10362892
Publication No. US2004003881A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-362-892-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 EHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 EHYVDLKDRPFFAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPCTIRGDFC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030207299A1 7274927CD1
                                                                                                                                                                                        APPLICANT: MALLIA, Natinder K.; HAPALIA, April J.A.;
APPLICANT: WALLIA, Natinder K.; HAPALIA, April J.A.;
APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
APPLICANT: GURURAJAN, Rajagopal: DING, Li;
APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
APPLICANT: THORWYON, Michael, ELLIOTT, Vicki S.;
APPLICANT: THORWYON, Michael, ELLIOTT, Vicki S.;
APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;
APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.;
APPLICANT: KEANNEY, Liam; POLICKY, Jennifer L.;
APPLICANT: THANGAVELU, Kavitha; BURFORD, Neil
TITLE OF INVENTION: HUMAN KINASES
CURRENT APPLICANT: PRANCAVELU, Kavitha; BURFORD, Neil
FILE REFERENCE: PI-0209 USA
CURRENT APPLICANT: MINDER: US/10/288,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 IQVGRNIIHGSDSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 IQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 88.4%; Score 774.5; DB 4; Best Local Similarity 90.2%; Pred. No. 5.8e-77; Matches 147; Conservative 4; Mismatches 11;
            121 DSVESAEKEISLWFQPEELVDYKSCAQNWIYE 152
                                                                                                             Sequence 19, Application US/10288798
Publication No. US20030207299A1
GENERAL INFORMATION:
APPLICANT: BANDMAN, Olga; NGUYEN, Danniel B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                            JS-10-288-798-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-288-798-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

RESULT 11 .US-10-362-892-19

```
64 EHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 PAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.4%; Score 774.5; DB 4; Length 177; 90.2%; Pred. No. 5.8e-77;
APPLICANT: INCYTE GENOMICS, INC.; BANDWAN, Olga
APPLICANT: NGUYEN, Danniel B.; WALIA, Narinder K.
APPLICANT: APPLICANT: CANDELLO AND THE CANDER GENOMICS APPLICANT: CANDELLO AND THE CANDER GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENOMICS GENO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040038881A1 7274927CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 IQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANI: BOKFOKD, WELL
CRREEN : BOKFOKD, WELL
CURRENT APPLICATION WUMBER: US/10/362,892
CURRENT APPLICATION WUMBER: US/10/362,892
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,873
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: US 60/232,654
PRIOR APPLICATION NUMBER: US 60/232,654
PRIOR PRILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/238,389
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: US 60/240,542
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13342, Application US/10732923
Ubblication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-10-732-923-13342
```

ઠે 셤 8 g à

```
75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 86.6%; Score 759; DB 4; Length 15
Best Local Similarity 94.1%; Pred. No. 2.4e-75;
Matches 143; Conservative 3; Mismatches 6; Indels
                                                                                                                                           Sequence 4, Application US/10232188
Publication No. US20030022306A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                     ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/713,825
PILING DATE: «Unknown»
ATTORNEY/AGENI INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 152
121 DSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,188
FILING DATE: 28-Aug-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE: 468542
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 11, Application US/10133628
; Publication No. US20030207830A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 152 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-10-133-628-11
                                                                                                                         US-10-232-188-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-232-188-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Penzberg, Jozn-Peter
APPLICANT: Goppelt, Andreas
APPLICANT: Goppelt, Andreas
APPLICANT: Goppelt, Andreas
APPLICANT: Goppelt, Andreas
APPLICANT: Regenbogen, Johannes
TITLE OF INVENTION: Use of polypeptides or nucleic acids
TITLE OF INVENTION: encoding these of the gene family NN23 for the diagnosis or
TITLE OF INVENTION: treatment of skin or intestinal disorders, and their use for
TITLE OF INVENTION: the identification of pharmacologically
TITLE OF INVENTION: active substances
FILE REFERENCE: 50125/012002
CURRENT APPLICATION NUMBER: US/09/791,118A
CURRENT FILING DATE: 2000-02-22
PRIOR FILING DATE: 2000-04-24
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PAGLVKYMISGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 EHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRPF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 PAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGPRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                        Length 177;
       TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.6%; Score 759; DB 3; Length 152; ilarity 94.1%; Pred. No. 2.4e-75; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                        11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 IQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 IQVGRNIIHGSDSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 177
                                                                                                                                                                                                                                                                                                                        DB 5;
                                                                                                                                                                                                                                                                                                                     Score 774.5; DB 5
Pred. No. 5.8e-77;
4; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                         FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 13342
LENGTH: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09791118A Patent No. US20020034741A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.2%;
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Werner, Sabine APPLICANT: Braun, Susanne
                                                                                                                                                                                                                       TYPE: PRT
CRCANISM: Homo sapiens
US-10-732-923-13342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-791-118A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-791-118A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 152
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 1
```

ö

9

용

ò 셤

APPLICANT: GALLOIS-MONTBRUN, SARAH

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SCHNEIDER, BENOIT
APPLICANT: SCHNEIDER, BENOIT
APPLICANT: GIACOMONI-FERNANDES, VERONIQUE
APPLICANT: DEVILLE-BONNE, DOMINIQUE
APPLICANT: DEVILLE-BONNE, DOMINIQUE
TITLE OF INVENTION: MUTANT NDP KINASES FOR ANTIVIRAL NUCLEOTIDE ANALOG
TITLE OF INVENTION: ACTIVATION AND THERAPEUTIC USES THEREOF
FILE REFERENCE: 03495.0227-00000
CURRENT APPLICATION NUMBER: US/10/133,628
CURRENT APPLICATION NUMBER: US/10/133,628
CURRENT PILING DATE: 2002-04-29
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
TYPE: PRT
TYPE: PRT
CORGANISM: Homo sapiens
US-10-133-628-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRPF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 MANSERTFIAIKPDGVQRGLVGBIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 86.6%; Score 759; DB 4; Length 152; Best Local Similarity 94.1%; Pred. No. 2.4e-75; Matches 143; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 DSVKSAEKEISLWFQPBELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
```

Search completed: December 16, 2005, 17:01:36 Job time : 118.453 secs

```
US-08-713-825-5
Sequence 5, Appli
Sequence 1, Appli
Sequence 987, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 633, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5, Appli
1, Appli
2, Appli
3, Appli
3, Appli
3, Appli
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Appl
Sequence 18029, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Appli
                                                                  December 16, 2005, 16:31:59 ; Search time 31.5472 Seconds (without alignments) 398.346 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-551-974A-20
US-09-565-501A-20
US-09-639-206A-20
US-09-874-923-20
US-08-798-841-20
US-09-248-796A-18029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-335-948-5
US-09-335-948-5
US-09-513-9905-5323
US-08-67-023-2
US-08-13-825-3
US-09-199-842-3
US-09-160-532-3
US-09-183-861-20
US-09-183-861-20
US-09-022-765-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-335-948-2
US-07-806-9338-3
US-08-113-825-4
US-09-199-842-4
US-09-35-948-4
US-09-538-092-933
                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-460-532-5
US-09-538-092-987
                                                                                                                                                                                  572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                           Listing first 45 summaries
                                                 OM protein - protein search, using sw model
                                                                                                                                                              Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                               Issued_Patents_AA:*
                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
                                                                                                             US-10-074-694-5
                                                                                                                                                    BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0
100.0
100.0
100.0
89.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88333386.55
                                                                                                                        Perfect score:
                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                 Sequence:
                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                               Database
                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
80
```

```
ö
             Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 59, Appli
Sequence 31, Appli
Sequence 91, Appli
Sequence 91, Appli
Sequence 91, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 7960, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 803; DB 1; Length 152; 100.0%; Pred. No. 1.6e-91; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                    US-08-713-825-5
Sequence 5, Application US/08713825
Sequence 5, Application US/08713825
Sequence 5, Application:
Sequence 5, Application:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
MEDIUM SYSTEM: DOS
SOFTWARE: FastSEQ Vereion 1.5
CURRENT APPLICATION NUMBER: US/08/713,825
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER: MEDIUM DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: MAMER: BILLINGS, LUCY J. REGISTRENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
  COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: Generation 127983
  STRANDEDNESS:
```

```
121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                吕
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                61 FPGLVKYWNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 PPGLVKYMNSGPVVAMVWEGLANVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIOVGRNIIHGS 120
                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                    9
                      1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                            61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 803; DB 2; Length 152; 100.0%; Pred. No. 1.6e-91; Live 0; Mismatches 0; Indels
                                                                                                                                                            RESULT 2

RESULT 2

US-09-199-842-5

Squence 5, Application US/09199842

Patent NO. 6087125

GENERAL INFORMATION:
APPLICANT: Bandman, Olga

APPLICANT: Bandman, Olga

APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION:
OGRESSES:
CORRESSES:
ADDRESSE:
STREET: 3174 Porter Pharmaccuticals, Inc.
STREET:
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                        121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
TELECOMMINICATION INFORMATION:
TELEFAX: 415-855-0555
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,842
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,825
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 152, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIAL
LIBRARY: General
March 127983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; CLONE: 1
US-09-199-842-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                            ò
                                                                                                                 셤
                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                       APPLICANT: Charles N. King
APPLICANT: Charles N. King
APPLICANT: Charles S. Steeg
APPLICANT: Lacta S. Steeg
APPLICANT: Lacta S. Steeg
TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
TITLE OF INVENTION: AND ANTIBODIES THEREFOR
FILE REPRENCE: 14014.0321
CURRENT APPLICATION NUMBER: US/09/335,948
CURRENT PILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 09/475,634
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/806,932
PRIOR FILING DATE: 1991-12-11
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 6
SOFWMARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-460-532-5
Sequence 5, Application US/09460532
Sequence 10. 648630
GENERAL INFORMATION:
GENERAL INFORMATION:
Hawkins, Phillip R.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 803; DB 2;
100.0%; Pred. No. 1.6e-91;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,532
FILING DATE: 13-Dec-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5
                                                                                                                          of Health
                                              ; Sequence 1, Application US/09335948; Patent No. 6329108
GENERAL INFORMATION:
APPLICANT: National Institutes of 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CA
RESULT 3
US-09-335-948-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-335-948-1
```

```
Sequence 2, Application US/09335948
Patent No. 6129198
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-806-932B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-335-948-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                 원
                                                                                                                                                              ઠે
                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 987, Application US/09538092

Sequence 987, Application US/09538092

Betent No. 6753314

GENERAL INFORMATION:

APPLICANT: Giot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

TILE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT PILING DATE: 1999-04-01

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR PILING DATE: 1999-04-01

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CURAPALSEGFFORMATTER VERSION 0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEBHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 803; DB 2; Length 152; Best Local Similarity 100.0%; Pred. No. 1.6e-91; Matches 152; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (0)...(0); OTHER INFORMATION: Polypeptide Accession Number P22392 US-09-538-092-987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 803; DB 2;
Pred. No. 1.6e-91;
                            FILING DATE: <Unknown>
APPLICATION NUMBER: 08/713,825
FILING DATE: <Unknown>
ATTORNEY/AGENT INPORMATION:
NAME: Bilings, Lucy J.
REGISTATION NUMBER: PF-0124 US
REPERENCE/DOCKET NUMBER: PF-0124 US
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-845-0555
TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 DSVKSAEKBISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
         APPLICATION NUMBER: US/09/199,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                    LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 152; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: GenBank
CLONE: 127983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: (0)...(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-460-532-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 987
```

쉽

유

8

g

ò

1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                           61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 FPGLVKYMNSGPVVAMVWEGLANVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 144
61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 MANLERTFIAIKPDGVQRGLVGEIIKRFEQXGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Charles R. King
APPLICANT: Charles R. King
APPLICANT: Charles R. King
APPLICANT: Charles R. King
APPLICANT: Particia S. Steeg
APPLICANT: Lance A. Liotta
TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
TITLE OF INVENTION: AND ANTIBODIES THEREFOR
TITLE OF INVENTION: AND ANTIBODIES THEREFOR
CURRENT APPLICATION NUMBER: US/09/335,948
CURRENT PILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/475,634
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1991-12-11
PRIOR APPLICATION NUMBER: 07/422,801
PRIOR FILING DATE: 1991-10-18
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PASISED for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRODUCTION AND USE OF HUMAN
HUMAN NM23 PROTEIN AND ANTIBODIES
THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/07806932B

Patent No. 6423836

GENERAL INFORMATION:
APPLICANT: KING, ET AL.
ITLE OF INVENTION: PRODUCTION AND USE OF HUMAN
ITILE OF INVENTION: THEREFOR
INTER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 803; DB 2;
; Pred. No. 1.9e-91;
0; Mismatches 0;
                                                                                                                                               121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 176
                                                                                                             121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
```

```
61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09199842
Patent No. 6087125
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Philip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.2%; Pred. No. 3.2e-81;
Matches 134; Conservative 10; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 DSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
APPLICATION NUMBER: US/08/713,825
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J6,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 12.000
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
TELECHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
                                                                                                                                                                                         PF-0124 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SUFURARE: PASTEGO VETSION 1.5
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,825
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               u.s.
                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE: 468542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ర
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-713-825-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-09-199-842-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 803; DB 2; Length 176; Best Local Similarity 100.0%; Pred. No. 1.9e-91; Matches 152; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08713825
Fatent No. 5874285
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3:FROM -24 TO 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                             CURRENT APPLICATION DATA:

SOFTWARE: DW4.V2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/806,932B

FILING DATE: 11 december 1991

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/422,801

FILING DATE: 18 october 1989

ATTORNEY/AGENT INFORMATION:

NAME: CAPELLO, SUSAN A.

REGISTRATION NUMBER: 34,560

REFERENCE/DOCKET NUMBER: 469200-72

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION SOFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 176 AMINO ACID RESIDUES AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-806-9328-3
                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE: HUMAN NM 23-H2S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: PROTEIN HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: SINTOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              u.s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-713-825-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
```

g

ద ò

Gaps

. 0

```
121 DSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 933, Application US/09538092
                                                                                                                          Sequence 4, Application US/09460532 Patent No. 6486300 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 152 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          468542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
US-09-538-092-933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-460-532-4
                                                                                                          US-09-460-532-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FAGLVKYMHSGPVVAMVWEGLANVVKTGRVMLGETNFADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MANLERTFIAIKPDGVQRGLVGBIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                        1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 89.7%; Score 720; DB 2; Length 152; Best Local Similarity 88.2%; Pred. No. 3.2e-81; Matches 134; Conservative 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                       Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF HUMAN NM23 PROTEIN
                                                                                                                                                                                                                                                                                                                                                              8; Indels
                                                                                                                                                                                                                                                                                                                   ; Score 720; DB 2;
; Pred. No. 3.2e-81;
10; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Charles R. King
APPLICANT: Charles R. King
APPLICANT: Charles R. King
APPLICANT: Patricia S. Steeg
APPLICANT: Lance A. Liotta
APPLICANT: Lance A. Liotta
TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN
TITLE OF INVENTION: AND ANTIBODIES THEREFOR
FILE REPERBENCE: 14014.0321
CURRENT APPLICATION NUMBER: US/09/335,948
CURRENT FILING DATE: 1999-06-18
PRIOR PILING DATE: 1995-06-17
PRIOR APPLICATION NUMBER: 07/806,932
PRIOR FILING DATE: 1991-12-11
PRIOR FILING DATE: 1991-12-11
PRIOR FILING DATE: 1999-10-18
NUMBER OF FILING DATE: 1999-10-18
SOFTWARE: FREUGE DATE: 1989-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 DSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-335-948-4
; Sequence 4, Application US/09335948
; Patent No. 6329198
; GENERAL INFORMATION:
      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                     89.78;
                          TELEPHONE: 415-855-0555
TELEPAX: 415-85-4166
INPORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 88.28
Matches 134; Conservative
                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                        CLONE: 468542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 152
                                                                                                                                                                                                                                                                            US-09-199-842-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-335-948-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                       Query Match
```

셤 ઠ ద

a ð

```
61 FAGLVKYMHSGPVVAMVWEGLAVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
APPLICANT: Bandman, Olga
Hawkins, Phillip R.
TILLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 89.7%; Score 720; DB 2; Best Local Similarity 88.2%; Pred. No. 3.2e-81; Matches 134; Conservative 10; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IEM Compatible
COMPUTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFTWARRE: FastSEQ Version 1.5
SOFTWARRE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,532
PILING DATE: 13-Dec-1999
PRIOR APPLICATION NUMBER: US/09/199,842
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US/09/199,842
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US/09/199,842
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERRENCE/DOCKET NUMBER: 9F-0124 US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 4:
```

ö

9 9

> 셤 δ 유

```
61 PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                 61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                           93 FAGLVKYMHSGPVVAMVWEGLAVVKTGRVWLGETNPADSKPGTIRGDFCIQVGRNIHGS 152
1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.7%; Score 720; DB 2; Length 184;
88.2%; Pred. No. 4.2e-81;
tive 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/07806932B
Patent No. 6423836
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN
TITLE OF INVENTION: HUMAN NM23 PROTEIN AND ANTIBODIES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI & STEWART
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                    121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                    153 DSVESAEKEIGLWFHPEELVDYTSCAONMIYE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION:
PUBLICATION INFORMATION: 1: FROM -32 TO 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/806,932B
FILING DATE: 11 december 1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,801
FILING DATE: 18 october 1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 184 AMINO ACID RESIDUES
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN NM 23-H28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: CAPELLO, SUSAN A.
REGISTRATION NUMBER: 34,560
REFERENCE/DOCKET NUMBER: 4692
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.24
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROSELAND
: NEW JERSEY
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 07068
                                                                                                                                                                                                                                                                                                                                RESULT 14
US-07-806-932B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NI
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                               셤
                                                                                                   ઠે
                                                                                                                                                셤
                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                    APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same;
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: 040/09/538,092
CURRENT PILING DATE: 2000-03-29
PRIOR PILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 933
LENGTH: 152
TYPE: PRT
ORGANISM: Homo sapiens
FRATURE:
CORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-04535-948-5

Sequence 5, Application US/09335948

Patent No. 65, Application US/09335948

GENERAL INFORMATION:
APPLICANT: Charles R. King
APPLICANT: Charles R. King
APPLICANT: Patricia S. Steeg
APPLICANT: AND ANTIBODIES THEREFOR
FILE REFERENCE: 14014.0321
CURRENT APPLICATION: AND ANTIBODIES THEREFOR
FILE REFERENCE: 14014.0321
CURRENT APPLICATION NUMBER: US/09/335,948
FRIOR FILING DATE: 1995-06-07
PRIOR PAPLICATION NUMBER: 07/806,932
PRIOR FILING DATE: 1999-12-11
PRIOR FILING DATE: 1999-10-18

NUMBER OF SEQ ID NOS: 6
SOFTWARER FRAESEQ for Windows Version 4.0

SECTION 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

89.7%; Score 720; DB 2; Length 184;
Best Local Similarity 88.2%; Pred. No. 4.2e-81;
Matches 134; Conservative 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (0)...(0)
CTHER INFORMATION: Polypeptide Accession Number P15531
US-09-538-092-933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 89.7%; Score 720; DB 2; Best Local Similarity 88.2%; Pred. No. 3.2e-81; Matches 134; Conservative 10; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

상 원 Search completed: December 16, 2005, 16:38:13 Job time: 32.5472 secs

This Page Blank (uspin)

```
RESULT 1
US-09-335-948-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-335-948-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Appli
...ce 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3, Appli
5, Appli
1, Appli
1, Appli
2, Appli
3, Appli
3, Appli
3, Appli
3, Appli
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20, Appl
20,
                                                                                                                                                                      (without alignments)
398.346 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                            December 16, 2005, 16:31:59 ; Search time 34.4528 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, p
Sequence 1, p
Sequence 5, p
Sequence 987,
Sequence 3, p
Sequence 3, p
Sequence 3, p
Sequence 3, p
Sequence 532, p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5,
                                                                                                                                                                                                                                                                                           1 QSQPAVKPCHLKGTMANSER......WFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-335-948-4
US-09-335-948-4
US-09-38-092-933
US-09-38-092-933
US-09-38-092-933
US-09-38-5-5
US-09-199-842-5
US-09-335-948-1
US-09-335-948-1
US-09-538-092-987
US-09-67-023-2
US-09-199-842-3
US-09-199-842-3
US-09-113-980-133
US-09-213-990-133
US-09-213-990-133
US-09-213-990-133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-022-765-20
US-09-551-974A-20
US-09-565-501A-20
US-09-639-206A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-874-923-20
US-08-798-841-20
                                                                                                                                                                                                                                                                                                                                                                                                                      572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                           US-10-074-694-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                                                                                                                                                                                                                                                              BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.2
62.5
62.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ritle:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š.
```

```
28 492 56.2 153 2 US-09-538-092-491 Sequence 491, Appl 30 481 54.9 187 2 US-09-13-825-1 Sequence 1, Appli 30 481 54.9 187 2 US-09-109-842-1 Sequence 1, Appli 31 481 54.9 187 2 US-09-460-532-1 Sequence 1, Appli 32 US-09-8538-032-823 Sequence 1, Appli 32 US-09-8538-032-823 Sequence 1, Appli 33 475 53.9 158 2 US-09-134-09 Sequence 59, Appli 34 466 53.2 231 2 US-09-134-01C-3216 Sequence 59, Appli 35 394 45.0 161 2 US-09-134-01C-3216 Sequence 32.6, Appli 37 394 45.0 161 2 US-09-134-01C-3216 Sequence 32.6, Appli 37 394 45.0 161 2 US-09-131-3645 Sequence 31, Appli 37 394 45.0 161 2 US-09-107-413-3645 Sequence 31, Appli 38 39.7 137 2 US-09-583-110-3639 Sequence 3645, Appli 320 36.5 145 2 US-09-107-433-3645 Sequence 1, Appli 44 308.5 35.2 200 2 US-09-902-540-10381 Sequence 10381, Appli 45 307 35.0 153 2 US-09-252-991A-22989 Sequence 22989, Appli 320 36.5 145 2 US-09-322-9914-10381 Sequence 22989, Appli 320 35.3 2 US-09-322-9914-10381 Sequence 22989, Appli 320 35.3 2 US-09-322-9914-2989 Sequence 22989, Appli 320 35.3 2 US-09-322-9914-2989 Sequence 22989, Appli 320 35.3 2 US-09-322-9914-2989 Sequence 22989, Appli 320 35.3 2 US-09-322-9914-2989 Sequence 22989, Appli 320 35.3 2 US-09-322-9914-2989 Sequence 7960, Appli 320 335-948-5
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 KEHYVDLKDRPFFFAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 QPQFKPKQLEGTWANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 QPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Sequence 5, Application US/09335948

Patent No. 6329198

GENERAL INFORMATION:
PAPPLICANT: National Institutes of Health
APPLICANT: Charles R. King
APPLICANT: Lance A. Liotta
TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
TITLE OF INVENTION: PRODUCTION AND ANTIBODIES THEREFOR
TITLE OF INVENTION: PRODUCTION AND ANTIBODIES THEREFOR
TITLE OF INVENTION NUMBER: US/09/335,948
CURRENT FILING DATE: 1999-06-18
PRIOR PRILING DATE: 1999-06-18
PRIOR PRILING DATE: 1999-06-18
PRIOR PLILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: 07/806,932
PRIOR FILING DATE: 1999-112-11
PRIOR APPLICATION NUMBER: 07/422,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 794; DB 2; Length 184;
Pred. No. 2.4e-85;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-07-806-932B-1
; Sequence 1, Application US/07806932B
; Patent No. 6423836
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 90.6%;
Best Local Similarity 91.5%;
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo Sapiens
```

```
STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-713-825-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-09-199-842-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 QPQFKPKQLEGTWANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFWQASEDLL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 OPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.6%; Score 794; DB 2; Length 184; Best Local Similarity 91.5%; Pred. No. 2.4e-85; Matches 150; Conservative 4; Mismatches 10; Indels
APPLICANT: KING, ET AL.

TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN
TITLE OF INVENTION: HUMAN NM33 PROTEIN AND ANTIBODIES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARCLLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CARCLLIA, BYRNE, BAIN, GILFILLAN,
CITTE: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 CIQVGRNIIHGSDSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION:
PUBLICATION INFORMATION: 1: FROM -32 TO 152
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/806,932B
FILING DATE: 11 december 1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,801
FILING DATE: 18 october 1989
ATTONNEY,AGENT INPORMATION:
NAME: CAPELLO, SUSAN A.
REGISTRATION NUMBER: 34,560
REFREENCY INDOMEST: 34,560
REFREENCY INDOMEST: 34,560
TELECOMUNICATION INPORMATION:
TELECOMUNICATION INPORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1700
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 184 AMINO ACID RESIDUES
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DW4.V2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
ORIGINAL SOURCE: HUMAN NM 23-H28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08713825
Patent No. 5874285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: PROTEIN
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                        07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-806-932B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-08-713-825-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
61 FAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFWQASEDLLKEHYVDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 86.6%; Score 759; DB 1; Length 152; Best Local Similarity 94.1%; Pred. No. 2.4e-81; Matches 143; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESSED ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 152
                                                                                                                                                                            COMPUTER: IRM Compatible
COMPUTER: IRM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PRASEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,825
FILING DATE: Filed Herewith
PRICR APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF-0124 US
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-855-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09199842
Patent No. 6087125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIE. 34304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatibl
OPERATING SYSTEM: DOS
                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
STREET: 31/4 CTTY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: GenBa
                                                                                     u.s.
```

```
75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                         61 FAGLVKYMHSGFVVAMVWEGLANVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                          75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                       1 MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFWQASEDLLKEHYVDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 MANSERTFIAIKPDGVQRGLVGBIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                           15 MANSERTFIAIKPDGVQRGLVGEIIKRPEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPP
Gaps
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 86.6%; Score 759; DB 2; Length 152; Best Local Similarity 94.1%; Pred. No. 2.4e-81; Matches 143; Conservative 3; Mismatches 6; Indels
6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09460532
Patent No. 6486300
GENERAL INFORMATION
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/199,842
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/713,825
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0124 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                           135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                        121 DSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 152
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPBRATING SYSTEM: DOS
SOFTWARE: FRASEGO VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,532
FILING DATE: 13-Dec-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 152 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide
143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    u.s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE: 468542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.
                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-09-460-532-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-460-532-4
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                            셤
                                                                                                                                                                                        셤
                                                                                                                                                                                                                                              ò
                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FAGLVXYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MANCERTFIAIKPDGVQRGLVGEIIKRFEQXGFRLVGLKFMQASEDLLKEHYVDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 759; DB 2; Length 152; Pred. No. 2.4e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 759; DB 2; Length 152;
Pred. No. 2.4e-81;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: National Institutes of Health
APPLICANT: Charles R. King
APPLICANT: Charles R. King
APPLICANT: Patricia S. Steeg
APPLICANT: Lance A. Liotta
TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
TITLE OF INVENTION: AND ANTIBODIES THEREFOR
FILE REFERENCE: 14014.0321
CURRENT APPLICATION NUMBER: US/09/335,948
CURRENT PILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR PELING DATE: 1995-06-17
PRIOR PELING DATE: 1995-06-07
PRIOR PELING DATE: 1995-06-07
PRIOR PELING DATE: 1991-12-11
PRIOR PELING DATE: 1991-12-11
PRIOR PELING DATE: 1989-10-18
PRIOR PELING DATE: 1989-10-18
PRIOR FILING DATE: 1989-10-18
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION UNBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0124 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                      APPLICATION NUMBER: US/09/199,842 FILING DATE:
                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,825
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09335948
Patent No. 6329198
  FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.6%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 94.1%;
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    468542
```

LIBRARY:

; US-09-199-842-4

75

8

ઠ

135

8

9

LENGTH: 152 TYPE: PRT

SEO ID NO 4

ö

83

```
SOFTWARE: FastSEQ for Windows Version 4.0
                        SEQ ID NO 2
LENGTH: 176
TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-07-806-932B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                        US-09-335-948-2
                                                                                                                                                                                                                                                                                                             ద
                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
61 FAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FAGLVKYMHSGPVVAMVWEGLAVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                      APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same;
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR PILING DATE: 1990-04-01
PRIOR PILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CLTAPARE: CLTAPARESCHORMATEET VERSION 0.9
SEG ID NO 933
LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFMQASEDLLKEHYVDLKDRPF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 FIGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 86.6%; Score 759; DB 2; Length 152; Best Local Similarity 94.1%; Pred. No. 2.4e-81; Matches 143; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Charles R. King
APPLICANT: Patricia S. Steeg
APPLICANT: Dance A. Liotta
TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
TITLE OF INVENTION: AND ANTIBODIES THEREFOR
FILE REFERENCE: 14014.0321
CURRENT APPLICATION NUMBER: US/09/335,948
CURRENT FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature

: LOCATION: (0)...(0)

: OTHER INFORMATION: Polypeptide Accession Number P15531

US-09-538-092-933
                                                                                               135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 DSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NS-09-335-948-2

Sequence 2, Application US/09335948

Patent NO. 6329198

; GENERAL INFORMATION:

; APPLICANT: National Institutes of Health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 08/475,634
PRIOR FILING DATE: 1955-06-07
PRIOR APPLICATION NUMBER: 07/806,932
PRIOR FILING DATE: 1991-12-11
PRIOR APPLICATION NUMBER: 07/422,801
PRIOR FILING DATE: 1989-10-18
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                   Sequence 933, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                  US-09-538-092-933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                          셤
                                                                       ò
                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
84 FFPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                           74 FFIGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHG 133
                                                                                                                                                                                                                                                                                   24 TWANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAWKFLRASEEHLKQHYIDLKDRP
                                                                                                                                                                                                                                14 TMANSERTFIAIKPDGVORGLVGEIIKRFEOKGFRLVGLKFLQASEDLLKEHYTDLKDRP
                                                                                                                           Gaps
                                                                                                                           .
0
83.8%; Score 734; DB 2; Length 176; 90.2%; Pred. No. 2.7e-78; Live 9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/07806932B
; Sequence 3, Application US/07806932B
; GENERAL INFORMATION:
TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN
; TITLE OF INVENTION: HUMAN NM23 PROTEIN AND ANTIBODIES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,
ADDRESSEE: CRECHI & STEWART
; STREET: CECCHI & S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RELEVANT RESIDUES IN SEQ ID NO: 3:FROM -24 TO 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 SDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 SDSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DW4.V2
CURRENT APPLICATION UNDER: US/07/806,932B
FILING DATE: 11 december 1991
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,801
FILING DATE: 18 october 1989
ATTORNEY/AGENT INFORMATION:
NAME: CAPELLO, SUSAN A.
REGISTRATION NUMBER: 34,560
REFERENCE/DOCKET NUMBER: 469200-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 176 AMINO ACID RESIDUES
AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
ORIGINAL SOURCE: HUMAN NM 23-H2S
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3:
     Query Match
Best Local Similarity 90.29
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: PROTEIN HYPOTHETICAL: NO
```

```
75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FPGLVKYMNSGPVVAMVWEGLANVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                   61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 729; DB 2; Length 152;
Pred. No. 8.4e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                 US-09-199-842-5

Sequence 5, Application US/09199842

Patent No. 6087125

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Hawkins, Phillip R.

TITLE OF INFURITION: NOVEL HUMAN NM23-LIKE PROTEIN

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: ADDRESSE:

ADDRESSEE: ADDRESSE:

CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                  121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0124 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOSS SOFTWARE: FASTSEQ VERSION 1.5 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/199,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,825
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-0124
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 152 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.1;
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            u.s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: GenBa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-199-842-5
                                                                               135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                               셤
                                      셤
                                                                               ò
                                                                               ö
                                                                                                                                                                                                                                 84 FFPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHG 143
                                                                                                                                                                                                        74 FFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHG 133
                                                                                                                                                                 83
                                                                                                                                                24 TWANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                        14 TMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                 Gaps
                                                                                 ;
0
                                    Length 176; •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 83.2%; Score 729; DB 1; Length 152; Best Local Similarity 90.1%; Pred. No. 8.4e-78; Matches 137; Conservative 9; Mismatches 6; Indels
                                                                               6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08713825
Patent No. 5874285
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                      Score 734; DB 2;
Pred. No. 2.7e-78;
9; Mismatches 6
                                                                                                                                                                                                                                                                                         134 SDSVKSAEKEISLWFOPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                               144 SDSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1074e Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: U.S. ZTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0124 US
TELECHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 5.
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,825
FILING DATE: Filed Herewith
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                      Query Match
Best Local Similarity 90.2%;
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: li
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94304
  US-07-806-932B-3
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-08-713-825-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-713-825-5
                                                                                                                                                                 ď
                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.19
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                     LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-538-092-987
                                                                                                                                                                                                                                                                                                                                                                                 US-09-460-532-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVWLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                      APPLICANT: National Institutes of Health
APPLICANT: Charles R. King
APPLICANT: Charles R. King
APPLICANT: Charles R. King
APPLICANT: Dance A. Liotta
TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN NM23 PROTEIN
TITLE OF INVENTION: AND ANTIBODIES THEREFOR
TITLE OF INVENTION: AND ANTIBODIES THEREFOR
TITLE OF INVENTION: AND ANTIBODIES THEREFOR
TITLE OF INVENTION: AND ANTIBODIES THEREFOR
TITLE OF INVENTION: AND ANTIBODIES THEREFOR
TITLE OF INVENTION: 1999-06-18
CURRENT APPLICATION NUMBER: 08/09/335,948
PRIOR APPLICATION NUMBER: 07/806,932
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/422,801
PRIOR FILING DATE: 1989-10-18
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 1
LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09460532
Patent No. 6486300
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 729; DB 2;
Pred. No. 8.4e-78;
9; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 DSVKSAEKEISLWFKPEBLVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460, 532
FILING DATE: 13-Dec-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/199,842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: <Unknown>
APPLICATION NUMBER: 08/713,825
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 Porter Drive
CITY: Palo Alto
             Sequence 1, Application US/09335948
Patent No. 6329198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.2%;
90.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.15
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-09-460-532-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-335-948-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

```
61 FPGLVKYMNSGPVVAMVWEGLAVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 987, Application US/09538092

Sequence 987, Application US/09538092

Patent No. 6753314

GENERAL INFORMATION:

APPLICANT: Give, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

FILE REFERENCE: 15966-542

CURRENT FILING DATE: 2000-03-29

FILOR APPLICATION NUMBER: 60/127,352

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR PLING DATE: 1999-04-01

PRIOR PLING DATE: 1999-04-01

PRIOR PLING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CURAPACESCOFORMATTER VERSION 0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 MANSERTFIAIKPDGVORGLVGEIIKRFEOKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.2%; Score 729; DB 2; Length 152;
90.1%; Pred. No. 8.4e-78;
tive 9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.2%; Score 729; DB 2; Length 152;
90.1%; Pred. No. 8.4e-78;
ive 9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature

: LOCATION: (0)...(0)

: OTHER INFORMATION: Polypeptide Accession Number P22392

US-09-538-092-987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE,DOCKET NUMBER: PF-0124 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE: 127983
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                           LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                               TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
```

ö

```
61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCLQVGRNIHGS 120
                                                                                                                                                                                                                        Sequence 2, Application US/08667023
; Sequence 2, Application US/08667023
; Patent No. 5817783
; Patent No. 5817783
; Patent No. 5817783
; Patent No. 5817783
; Patent No. 58177831
; APPLICANT: Callabreta, Bruno
; APPLICANT: Martinez, Robert V.
; TITLE OF INVENTION: DR-nm23 AND COMPOSITIONS, METHODS OF MAKING AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5817783ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 ERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPFFTGL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 ERTFLAVKPDGVQRRLVGEIVRRFERKGFKLVALKLVQSSEELLREHYAELRERPFYGRL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.5%; Score 547.5; DB 1; Length 168; 66.2%; Pred. No. 2.4e-56; Artive 32; Mismatches 17; Indels 1.
                                                                      141 SARREIALWFRADELLCWEDSAGHWLYE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 SAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: December 16, 2005, 16:38:12 Job time : 35.4528 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE:
CLASSIFICATION NOTES.
FILING DATE:
CLASSIFICATION ATS.
PRIOR APPLICATION DATA:
APPLICATION NOTES.
CLASSIFICATION DATA:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE DOCKET NUMBER: TJU-1992
REFERENCE DOCKET NUMBER: TJU-1992
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEG 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH 168 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZOPILIA: USAS
ZOPILIA: USAS
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDFAFFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.2*
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-667-023-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                  RESULT 15
US-08-667-023-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                           ò
                                                                                                                      g
```

This Page Blank (uspto)

```
NDKB_HUMAN
                                                                                                                                                                                                                                                                                                     P22392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ношо
                                                                                                                                                                                                                                                           RESULT
NDKB_HU
                                                                                                                                                                                                                                                                                           A PART OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRICE OF THE PRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xenopus lae
xenopus tro
xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pygma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pongo pygma
rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 columba liv
rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    canis famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ictalurus p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cavia porce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  brachydanio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gallus gall
canis famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bos taurus
bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bos taurus
                                                                                 December 16, 2005, 16:31:58 ; Search time 140.528 Seconds (without alignments) 763.122 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                       1 MANLERTFIAIKPDGVQRGL........WFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pongo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q6azk9 :
P70010 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P52174
Q56jv4
Q50ka9
P15531
Q6fgk3
Q5rc56
Q80vt7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q01768
Q5nc82
O57535
Q50ka8
Q90380
Q05982
P15532
Q5nc81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09ptf5
P70071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        099ni2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q5pq80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P70011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07sxg5
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                             2166443 seqs, 705528306 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDKA_BOVIN
Q56JV4_BOVIN
NDKA_CĀNFA
NDKA_HUMAN
Q6FGK3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSNCB2 MOUSE
OS7535 CHICK
QS0KA8 CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NDKA_MOUSE
QSNC81 MOUSE
NDKB_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PONPY
MOUSE
HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q5PQ80 XENLA
Q7SXG5 BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7SXG5_BRARE
Q9IAD3_BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q6FHN3_HUMAN
Q5RFH3_PONPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \overline{x}enla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XENTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDKB_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDKA1 XENLA
                                                                                                                                                                                                                                                                                                                                                                               Listing first 45 summaries
                                                         - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z6AZK9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q99NI2
                                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                         1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                           UniProt 05.80:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match Length DB
                                                                                                                                               US-10-074-694-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153
154
154
               Copyright
                                                                                                                                                                                                     BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1000.0
999.0
999.0
993.1
991.2
990.8
990.9
990.9
990.9
990.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.3
88.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.4
88.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                              Perfect score:
                                                         OM protein
                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š.
```

Q68fi7 xenopus lae O60361 homo sapien	P27950 ginglymosto O804v0 oncorhynchu	O57560 salmo salar	Qepcs/ brachydanio Q7sx14 brachydanio	Q7zzq7 oreochromis	P08879 drosophila	Q6xi71 drosophila	Q5nc80 mus musculu	Q7qix6 anopheles g	_	Q4t9n6 tetraodon n
Q68FI7 XENLA NDK8 HUMAN	NDK GINCI 0804Y0 ONCMY	057560_SALSA	Q6FC3/ BRARE Q7SXL4 BRARE	Q7ZZQ7_OREMO	NDKA DROME	NDKA DROYA	Q5NC80 MOUSE	Q7QIX6_ANOGA	Q8R4B4 MOUSE	Q4T9N6_TETNG
24	ч 0	000	7 (7	~	П	П	(1)	7	N	7
154	151	151	153	152	152	150	127	153	365	144
86.9	82.9	81.7	81.1 80.9	78.4	77.2	76.7	75.5	74.2	74.0	73.6
698 691	666	656	651 650	629.5	620	616	909	296	594	591
2 6	3.4	9 1	28.7	33	0	11	7	43	44	5

ALIGNMENTS

```
The STATE TO THE STANDARD;

TO TOWER HOWN.

TO TOWER THE STANDARD;

TO THE STANDARD THE STANDARD;

TO THE TAXTDARDARD THE STANDARD THE ST
```

metabolism;

```
<u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                          A TABLINE 963668; PubMed=8747457; DOI=10.1016/S0969-2126(01)00268-4;

A MEDLINE=9636368; PubMed=8747457; DOI=10.1016/S0969-2126(01)00268-4;

A Morera S., Lacombe M.-L., Xu Y., Lebras G., Janin J.;

"X-ray structure of human nucleoside diphosphate kinase B complexed
with GDP at 2-A resolution.";

Structure 3:1307-1314(1995).

- :- FUNCTION: Major role in the synthesis of nucleoside triphosphates
other than APP.

- :- FUNCTION: Acts as a transcriptional activator of the c-Myc gene;
binds DNA nonspecifically (Ref. 3).

- :- CATALYTIC ACTIVITY: APP + nucleoside diphosphate = ADP +
nucleoside triphosphate.

- :- COFACTOR: Magoresium (By similarity).

- :- SUBURIT: Hexamer of two different chains: A and B (A6, A5B, A4B2,
A3B3, A2B4, AB5, B6).

- :- SUBCLIULAR LOCATION: Nuclear and cytoplasmic.
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
                                                                                                                                                                                            MEDLINE=95387396; PubMed=7658474;
Webb P.A., Perisic O., Mendola C.E., Backer J.M., Williams R.L.;
"The crystal structure of a human nucleoside diphosphate kinase, NM23-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PTM: The N-terminus is blocked.
-!- DTMSTSASE: This protein is found in reduced amount in tumor cells of high metastasic potential.
-!- SIMILARITY: Belongs to the NDK family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MING, 10005634; C:nucleus; NAS.

GO; GO:0005524; F:ATP binding; NAS.

GO; GO:0005524; F:ATP binding; NAS.

GO; GO:0005524; F:ATP binding; NAS.

GO; GO:0003700; F:transcription factor activity; TAS.

GO; GO:0003700; F:transcription of cell proliferation; TAS.

GO; GO:0009142; P:negative regulation of cell proliferation; TAS.

R GO; GO:0009142; P:negulation of transcription, DNA-dependent; TAS.

R InterPro; IPR012005; NDK-2.

R Pfam; FP0034; NDK. 1.

R PRINTS; PR01243; NUCDPKINASE.

R PROMO: PR001018; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D-structure, Activator, Anti-oncogene, ATP-binding, Cell cycle, Direct protein sequencing, DNA-binding, Kinase, Magnesium,
                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X58965; CAB37870.1; -; mRNA.
EMBL; M56981; AAA36569.1; -; mRNA.
EMBL; L16785; AAA60228.1; -; mRNA.
EMBL; BC002476; AA402476.1; -; mRNA.
PIR; A49798; A49798.
PDB; INXE; X-ray; L/N/O/R/T/U=1-152.
PDB; INVE; X-ray; A/B/C/D/E/F=2-152.
TRANSFAC; T00706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ensembl; ENSG0000121054; Homo sapiens
                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00562; NDK; 1.
PROSITE; PS00469; NDP KINASES; 1.
3D-structure; Activator; Anti-ono
                                                                                                                                                                                                                                                                                      J. Mol. Biol. 251:574-587(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC; HGNC:7850; NME2.
H-InvDB; HIX0013993; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reactome; P22392; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 156491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OGP; P22392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              removed.
                                                                                                                                                                                                                                                                                                          9
      {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {f Z} {
```

```
FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PPGLVKYMNSGPVVAMVWEGLAVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                  Pros-phosphohistidine intermediate.
Substrate ATP/NDP ribose.
Substrate ATP/NDP base.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP base.
Substrate ATP/NDP ribose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
NME2 protein (Non-metastatic cells 2, protein (NM238) expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
NUCLEOTIDE SEQUENCE.Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150
17298 MW; 1A5C3F84D7AD272C CRC64;
Metal-binding, Nuclear protein; Nucleotide metabolis
Nucleotide-binding; Phosphorylation; Transcription;
Transcription regulation; Transferase.
ACT_SITE 118 118 Pros-phosphohistidine:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 803; DB 1;
Pred. No. 4.6e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; scc.
100.0%; Pred
0; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEFHN3_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 152; Conservative
                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         145
147
152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                    12
60
88
94
105
1112
1152
                                                                                                                                                                         113
118
118
1118
136
1110
1111
1112
136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=NME2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HELIX
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                      ACT SITE
BINDING
BINDING
BINDING
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                    BINDING
BINDING
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q6FHN3;
                                                                                                                                                           STRAND
HELLY
TURN
HELLY
TURN
TURN
HELLY
TURN
HELLY
TURN
HELLY
TURN
HELLY
TURN
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
HELLY
```

```
RESULT 3

COSREJO

OGSREJO

OT 01-FP

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
  ò
                                              g
                                                                                                                                                                                                                                                                                                                                TISSUB—Chondrosarcoma,

X Straubberg R.L., Peingold B.A., Grouse L.H., Derged J.G.,

Altaubberg R.L., Peingold B.A., Grouse L.H., Derged J.G.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haith F.,

Datchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

District Saraes M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rabey J., Helton E., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                          Shen B., Henze S., Mar W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BT007045; AAP35694.1; """."
EMBL; BT007045; AAP35694.1; "RNA.
EMBL; BC095458; AAH95458.1; -; mRNA.
ENSEMP. GOFHN3; 2-152.
ENSEMPL; ENGORO00121054; Home sapiens.
GO; GO:0016301; F:Kinase activity; IEA.
GO; GO:0016301; F:Kinase activity; IEA.
GO; GO:00164550; F:mucleoside-diphosphate kinase activity; IEA.
GO; GO:001641; P:CTP biosynthesis; IEA.
GO; GO:0006241; P:CTP biosynthesis; IEA.
GO; GO:0006288; P:UTP biosynthesis; IEA.
GO; GO:0006288; P:UTP biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 803; DB 2; Length 152; 100.0%; Pred. No. 4.6e-70; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Chondrosarcoma;
NIH MGC Project;
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
Neubert P., Kstrang K., Schatten R., Shen B., Henze S.,
Korn B., Zuo D., Hu Y., LaBaer J.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                            Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 AA; 17298 MW; 1A5C3F84D7AD272C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROSITE; PS00469; NDP_KINASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
SMART; SMO0562; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; CR541718; CAG46519.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.0
Matches 152; Conservative
                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

```
61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRLMLGETNFADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYTDLKDRPF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The German cDNA Consortium;
Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                    Pongo pygmaeus (Orangutan).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MANLERIFIAIXPDGVQRGIVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Nucleoside diphosphate kinase B (EC 2.7.4.6) (NDK B) (NDP kinase B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0005524; F:ATP binding; IEA.
GO:0016301; F:kinase activity; IEA.
GO:0016319; F:kinase activity; IEA.
GO:0016740; F:transferase activity; IEA.
GO:0016741; P:CTP biosynthesis; IEA.
GO:0006143; P:CTP biosynthesis; IEA.
GO:0006239; P:UTP biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
99.0%; Score 795; DB 2; Length 15
Best Local Similarity 98.7%; Pred. No. 2.8e-69;
Matches 150; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR857184; CAH89484.1; -; mRNA.
SMR; Q5RFH3; 2-152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00469; NDP_XINASES; 1.
Hypothetical protein.
SEQUENCE 152 AA; 17300 MW; 8D2D9361C94DC938 CRC64;
                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                    152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 AA
                            DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE
DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE
                                                                                                                                                                    PRT;
                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                             01-FEB-2005 (TrEMBLrel. 29, Created 01-FEB-2005 (TrEMBLrel. 29, Last se 01-FEB-2005 (TrEMBLrel. 29, Last se Hypothetical protein DKFZp468E0516, Name-DKFZp468E0516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDFKINASE.
ProDom; PD001018; NDK; 1.
SMART; SM00562; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
                                                                                                                                                                    QERFH3 PONPY PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Nme2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDKB RAT
P19804;
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                121
                                                                                                                                                PONPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (P18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDKB_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SE DI DI BE
```

ö

ö

Gaps

ö

9

1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF 1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF

ઠે 요 ઠ

PPGLVKXMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120

61

152 AA; 17283 MW; 1A5C3F84C1F413EC CRC64;

```
SEQUENCE
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                        NDKB MOUSE
                                                                                                          ò
                                                                                                                                          셤
                                                                                                                                                                            ò
                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley; TISSUE=Mast cell;
MEDLINE=92256389; PubMed=1316151;
Hemmerich S., Yarden Y., Pecht I.;
"A cromoglycate binding protein from rat mast cells of a leukemia line is a nucleoside diphosphate kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NITSOLITEMENT Gene Collection (MGC) project;
Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Major role in the synthesis of nucleoside triphosphates other than ATP. The ATP gamma phosphate is transferred to the NDP beta phosphate via a ping-pong mechanism, using a phosphorylated active-site intermediate.
-!- CATALTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleoside triphosphate.
--- COFACTOR: Magnesium (By similarity).
--- SUBUNIT: Hexamer of two different chains: A and B (A6, A5B, A4B2, A3B3, A2B4, AB5, B6).
--- SUBCELLULAR LOCATION: Cytoplasmic and plasma membrane.
                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.

BEDLINES-29232552: PubMed=1321145;

IShikawa N., Shimada N., Munakata Y., Watanabe K., Kimura N.;

"Isolation and characterization of a gene encoding rat nucleoside
                                                                                                                                                          Kimura N., Shimada N., Nomura K., Watanabe K.; "Isolation and characterization of a cDNA clone encoding rat nucleoside diphosphate kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SMO0562; NDK; 1.
SMOSTTE; PS00469; NDP KINASES; 1.
ATP-binding; Direct protein sequencing; Kinase; Magnesium;
Metal-binding; Nucleotide metabolism; Nucleotide-binding;
                                                                                                        NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> W (in Ref. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P22392; INUE.
SMR; P19804; 2-152.
Ensembl; ENSRNOG000000005671; Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: The N-terminus is blocked. SIMILARITY: Belongs to the NDK family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                   steoside diphosphate Kinase.";
Biol. Chem. 265:15744-15749(1990).
                                                                                                                                                                                                                                                                                                                     diphosphate kinase.";
J. Biol. Chem. 267:14366-14372(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M55331; AAA41684.1; -; mRNA.
EMBL; M91897; AAA42017.1; -; mRNA.
EMBL; BC086599; AAH86599.1; -; mRNA.
PIR; A41849; A38369.
HSSP; P22392; INUE.
                                                                                                                                          MEDLINE=90368787; PubMed=2168422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 31:4574-4579(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation, Transferase.
ACT_SITE 118 118
CONFLICT 89 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGD; 619877; Nme2.
InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
   Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE
                                                                  NCBI_TaxID=10116;
                                                                                                                             STRAIN=Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              removed.
```

```
ö
                                                                                                                                                                                                                                                61 PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                               61 PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANDIANAEL-2019 LONG TO TAKE THE TARGET OF THE TOWN TO SHARM THE TOWN TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN THE TOWN T
                                                                                                                                                            9
                                                                                                       1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                      1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQXGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Nme2;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   â
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92387389; PubMed=1325378; DOI=10.1016/0014-5793(92)80807-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (Rel. 25, Created)
1-APR-1993 (Rel. 25, Last sequence update)
10-WAY-2005 (Rel. 47, Last amocation update)
Nucleoside diphosphate kinase B (EC 2.7.4.6) (NDK B) (NDP kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Urano T., Takamiya K., Furukawa K., Shiku H.; molecular cloning and functional expression of the second mouse nm33/NDP kinase gene, nm23-W2."; FBS Lett. 309:358-362(1992).
                                                        .
0
98.9%; Score 794; DB 1; Length 152; 98.0%; Pred. No. 3.5e-69;
                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takeshi U.;
Submitted (SEP-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                     DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ā
                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                        Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6;
                            Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (nm23-M2) (P18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDKB MOUSE
                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takeshi
```

ŏ

```
WEDLINE-57BL/6; TISSUBERAIN, and Heart; WEDLINE-57BL/6; TISSUBERAIN, and Heart; WEDLINE-25BL/6; TISSUBERAIN, and Heart; WEDLINE-25BL/6; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bronstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Arabia S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Angewan P.J., McKernan K.J., Malek J.M., Gay L.J., Hulyk S.W., Angers R.M., Stableton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Miking M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Anthering M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Anthereffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Macherther M., Schein J.B., Jones B.J.M., Marra M.A., Schein J.B., Jones B.J.M., Marra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Major role in the synthesis of nucleoside triphosphates other than ATP. The ATP gamma phosphate is transferred to the NDP beta phosphate via a ping-pong mechanism, using a phosphorylated active-site intermediate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- COFACTOR: Magnesium (By similarity).
-!- SUBDNIT: Hexamer of two different chains: A and B (A6, A5B, A4B2, A3B3, A2B4, AB5, B6).
-!- SUBCELLULAR LOCATION: Cytoplasmic and plasma membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00469; NDP_KINASES; 1.
ATP-binding; Kinase; Magnesium; Metal-binding; Nucleotide metabolism; Nucleotide-binding; Phosphorylatlon; Transferase.
ACT_SITE 118 118 Pros-phosphohistidine intermediate (By
Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yashino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP nucleoside triphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC086892; AAH86892.1; ; mRNA.
EMBL; BC086893; AAH86893.1; -; mRNA.
PIR; S29241; S29241.
HSSP; P22392; INUE.
SMR; Q01768; 2-152.
SWISS-2DPAGE; Q01768; -
ENSEMD!, ENSWIGSO000020857; Mus musculus.
MGI; MGI:97356; Nme2.
GO; GO:005739; C:mitochondrion; IDA.
InterPro; IPR012005; NDK-2.

    -!- SIMILARITY: Belongs to the NDK family.

                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X68193; CAA48275.1; -; mRNA.
EMBL; AK012447; BAB28246.1; -; mRNA.
EMBL; BC066995; AAH6695.1; -; mRNA.
EMBL; BC086892; AAH86892.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PP00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCKPKINASE.
PRODOM; PD001018; NDK; 1.
SMART; SM00562; NDK; 1.
                                                                                                                                                                                 Nature 420:563-573(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     removed.
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                          61 PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                      PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                    1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                   1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASBEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASBEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ensembl; Party Company                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.8%; Score 793; DB 2; Length 152; 98.0%; Pred. No. 4.4e-69; ive 2; Mismatches 1; Indels
                                                                                     Length 152;
                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mashreghi-Mohammadi M.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; Al662838; CAI35363.1; -; Genomic_DNA.
SMR; QSNC82; 2-152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01243; NUCDPKINASE.
SMART; SM00562; NDK; 1.N.
PROSITE; PS00469; NDP KINASES; 1.
SEQUENCE 152 AA; 17363 MW; 1ASC3F84C1FFC83C CRC64;
                           152 AA; 17363 MW; 1A5C3F84C1FFC83C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-2005 (TrEMBLrel. 29, Last sequence update) 01-FEB-2005 (TrEMBLrel. 29, Last annotation update) Expressed in non-metastatic cells 2 protein. ORFMames=RP23-378113.2-002; Mus musculus (Mouse).
                                                                                  Score 793; DB 1;
Pred. No. 4.4e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 AA
                                                                                                                                             2; Mismatches
similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                     98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2005 (TrEMBLrel. 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSNC82_MOUSE PRELIMINARY;
QSNC82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.0°
Matches 149; Conservative
                                                                                                                                                Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1] T
NUCLEOTIDE SEQUENCE
                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                              SEQUENCE
                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

RESULT 7

```
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takahashi M., Une R., Fukushima K., Fujiki M., Misumi K., Miyoshi N., Endo Y., Oishi A., Akuzawa M.; "Molecular cloning of canine nm23 cDNAs and their expression in normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97450995; PubMed=9305928; DOI=10.1074/jbc.272.39.24604;
Lambeth D.O., Mehus J.G., Ivey M.A., Milavetz B.I.;
"Characterization and cloning of a nucleoside-diphosphate kinase
targeted to matrix of mitochondria in pigeon.";
J. Biol. Chem. 272:24604-24611(1997).
-! FINCTION: Major role in the synthesis of nucleoside triphosphates
other than ATP. The ATP gamma phosphate is transferred to the NDP
beta phosphate via a ping-pong mechanism, using a phosphorylated
active-site intermediate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate.
- nucleoside triphosphate.
- COPACTOR: Magnesium (By similarity).
- SUBCELLULAR LOCATION: Cytoplasmic and plasma membrane.
- ITSSUB SPECIFICITY: Highest levels in the liver and kidney with lower levels in the heart. brain and breast muscle.
- SIMILARITY: Belongs to the NDK family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Columba livia (Domestic pigeon).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
15-VUL-1998 (Rel. 36, Last sequence update)
10-WAY-2005 (Rel. 47, Last annotation update)
Nucleoside diphosphate kinase (EC 2.7.4.6) (NDF kinase)
                                                               and tumor tisuues.";
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AB207045; BAD97838.1; -; mRNA.
SMR; Q50KA8; 2-152.
                                                                                                                                                                                                                                                                                                        1.
923DA489B37C19C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                               93.4%; Score 750; DB 2;
92.1%; Pred. No. 6.7e-65;
ive 9; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 AA
                                                                                                                                                                                                                                                                                                    PROSITE; PS00469; NDP KINASES;
SEQUENCE 152 AA; 17366 MW;
                                                                                                                                                 InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
Pfam; PP00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDR(INASE.
ProDom; PD001018; NDK; 1.
SMART; SM00562; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                    93.4%;
                                                                                                                                                                                                                                                                                                                                                                                     st Local Similarity 92.1
tches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDK COLLI
Q90380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDK COLLI
        S DR DR DR TTA A S OR TTA A A S OR TTA A A S OR TTA A S
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 PGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFVHASEDLLKQHYIDLKDRPFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cantus ramiliaris (DOG).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ensembl; ENGGALGO000002932; Gallus gallus.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0016301; F:Kinase activity; IEA.

GO; GO:0004550; F:nucleoside-diphosphate kinase activity; IEA.

GO; GO:0006241; P:CTP biosynthesis; IEA.

GO; GO:0006228; P:CTP biosynthesis; IEA.

GO; GO:0006228; P:UTP biosynthesis; IEA.

InterPro; IPR012005; NDK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 751; DB 2; Lens-Pred. No. 5.4e-65; 4; Indels
                                                                                                                                                                                                                                                                                                                                            Mehus J.G., Lambeth D.O.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF043542; AAB99856.1; -; mRNA.
HSSP; P22392; INUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 AA; 17288 MW; 939DDD61D329E008 CRC64;
                                                               01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Nucleoside diphosphate kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.5%; Sco...
92.7%; Pred. No. 5...
7; Mismatches
                        153 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 SVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 SVESAQKEISLWFKPAELIDYRSCAHDWVYE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00469; NDP_KINASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERM; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDEKINASE.
ProDom; PD001018; NDK; 1.
SWART; SM00562; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSOKAB CANFA PRELIMINARY;
QSOKAB;
                        OS7535 CHICK PRELIMINARY;
0575357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 140; Conservative
                                                                                                                                                     Name=cNDPK;
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=nm23-C2;
                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
```

Kinase

g

g ò

ઠ ద

EMBL; U61287; AAC60275.1; -; mRNA.

NUCLEOTIDE SEQUENCE

NCBI_TaxID=9615;

RESULT 6

10 CSOKAB

10 CSOKAB

10 CSOKAB

11 CSOKAB

13 CSOKAB

13 CSOKAB

13 CSOKAB

13 CSOKAB

13 CSOKAB

13 CSOKAB

13 CSOKAB

14 CSOKAB

15 CSOKAB

16 CSOKAB

17 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

18 CSOKAB

1

CANFA

removed.

9

Gaps

.. 0

Length 152; Indels

```
the Buropean Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and this statement is
                                                                                                                                                                                ENSRNOG000000002693; Rattus
                                                                                    EMBL, D13374; BAA02635.1; -; mRNA.
PRF, A45208; A45208.
HSSP, P15531; 1JXV.
SMR; Q05982; 5-152.
                                                                                                                                                                                                                        GO; GO:0005813; C:centrosome; IDA.
InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                        Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Nme1; Synonyms=Nm23;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 90.19
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 342:177-180(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                        70497; Nme1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                Ensembl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                               removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDKA MO
P15532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDKA_MOUSE
                                                                                                                                                                                                        RGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HERER REPRESENTATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 PGLVKYMNSGPIVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCLQVGRNIHGSD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 ANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGMKFVHASEELLKQHYIDLKDRPFY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: Magnesium (By similarity).
-!- COFACTOR: Magnesium (By similarity).
-!- SUBDUNIT: Hexamer of two different chains: A and B (A6, A5B, A4B2, A3B3, A2B4, A8B, B6). Interacts with SET (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
-!- DISEABE: This procein is found in reduced amount in tumor cells of high metastasic potential.
-!- SIMILARITY: Belongs to the NDK family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kimura N.;
                  HSRP; P22392; INUE.
SMR; Q90380; 3-153.
InterPro; IPR01264; NDK.
InterPro; IPR012005; NDK.
InterPro; IPR012005; NDK.
PERM; PR00334; NDK; 1.
PRNST; PRSP00735; NDK; 1.
PRODOM; PD001018; NDK; 1.
PROSTE; PS00469; NDP KINASES; 1.
ATP-binding; Kinase; Magnesium; Metal-binding; Nucleotide metabolism; Nucleotide-binding; Phosphorylation; Transferase.
ACT_SITE 119 119 Prosp. Phosphorylation intermediate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase A)
(Tumor metastatic process-associated protein) (Metastasis inhibition factor NM23).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93155067; PubMed-8381409; Shimada N., Ishikawa N., Munakata Y., Toda T., Watanabe K., Kimura N. Shimada N., Ishikawa N., Munakata Y., Toda T., Watanabe K., Kimura N. Second form (beta isoform) of mucleoside diphosphate kinase from Tat. Isolation and characterization of complementary and genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                    Length 153;
                                                                                                                                                                                                                                                                                                                                                               Query Match
92.7%; Score 744; DB 1; Length 15
Best Local Similarity 90.7%; Pred. No. 2.6e-64;
Matches 137; Conservative 9; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                       4E245D7AE9F0C9EF CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 SVESAQKEINLWFKPAELIDFKSCAHDWIYE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 AA
    Genomic DNA
                                                                                                                                                                                                                                                                                                  similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
    EMBL; AF018266; AAC78437.1; -;
                                                                                                                                                                                                                                                                                                                       153 AA; 17299 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleoside triphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Nme1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          005982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDKA
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      원
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FSGLVKYMHSGPVVAMVWEGLAVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosengard A.M., Krutzsch H.C., Shearn A., Biggs J.R., Barker B., Margulies I.M.K., King C.R., Liotta L.A., Steeg P.S.; "Reduced Nm23/Awd protein in tumour metastasis and aberrant Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MANSERTFIAIKPDGVQRGLVGBIIKRFEQKGFRLVGLKFIQASEDLLKEHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                              1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase A)
(Tumor metastatic process-associated protein) (Metastasis inhibition factor NM23) (NDPK-A) (nm23-M1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
MEDLINE=88155671; PubMed=3346912;
Steeg P.S., Bevilacqua G., Kopper L., Thorgeirsson U.P.,
Talmadge J.E., Liotta L.A., Sobel M.E.;
Evidence for a novel gene associated with low tumor metastatic
potential.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                           91.2%; Score 732; DB 1; Length 152; 90.1%; Pred. No. 3.8e-63; ive 10; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
NUCLECTIDE SEQUENCE.
MEDLINE=90044071; Pubmed=2509941; DOI=10.1038/342177a0;
norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ą
```

```
MGI; MGI:97355; Nmel.
GO; GO:0005792; C:microsome; IDA.
GO; GO:0005625; C:soluble fraction; IDA.
                                                                    InterPro; IPR001564; NDK.
InterPro; IPR001564; NDK-2.
Pfam; PF000344; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCCPKINASE.
Probom; PD001018; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meth. Enzymol. 303:19-44(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSNC81 MOUSE PRELIMINARY;
OSNC81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 90.1
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [3]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                     Transferase.
                                                                                                                                                                                                                                                                                                                                                                  ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAINE-YERNY TISSUE-Mannary Jand;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausher R.D., Collins F.S., Wargner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan R.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Lakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Schnercation and initial analysis of more than 15,000 full-length human and mouse chan and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success and success 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISEASE: This protein is found in reduced amount in tumor cells of high metastasic potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91191558. PubMed=2013093; DOI=10.1016/0092-8674(91)90404-M; Leone A., Flatow U., King C.R., Sandeen M.A., Margulies I.M., Liotta L.A., Steeg P.S.; Redouced tumor incidence, metastatic potential, and cytokine responsiveness of mm23-transfected melanoma cells.";
                                                                                                                                                                                                                                                                                   STRAIN=129/Sv; Daniel J.Y.; Daniet S., Masse K., Daniel J.Y.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Swiss Webster / NIH;
Gervasi F., Fanciulli M., Lombardi D.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - SIMILARITY: Belongs to the NDK family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-2DPAGE; P15532; MOUSE.
Ensembl; ENSMUSG00000037601; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M35970; AAA39826.1; ALT_INIT; mRNA.
EMBL; M65037; AAA63391.1; -; mRNA.
EMBL; U85511; AAB42080.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
  Natl. Cancer Inst. 80:200-204(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF033377; AAB87689.1; -; mRNA.
EMBL; BC005629; AAH05629.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR, A46557, A46557.
HSSP, P15531, 1JXV.
SMR, P15532, 5-152.
                                                                                                                                                                                                                                      [4]
NUCLEOTIDE SEQUENCE
                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            removed.
```

```
61 PPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FTGLVKYMHSGPVVAMVWEGLAVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Expressed in non-metastatic cells 1 protein (12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430059B17 product:expressed in non-metastatic cells 1, protein (NW23A) (nucleoside diphosphate kinase), full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORFNames=RP23-378113.1-001;
Mus musculus (Mouse).
Eukarrota; Matazao; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/6J;
TISSUB-Embryonic body between diaphragm region and neck;
TISSUB-Embryonic body between diaphragm region and neck;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CS7BL/6J;

128SUBE-BADTyonic body between diaphragm region and neck;
MEDLINE=LD1085660; PubMed=11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
SMART; SM05562; NDK; 1.
PROSITE; PS00469; NDP KINASES; 1.
ATP-binding; Kinase; Magnesium; Metal-binding; Nuclear protein;
Nucleotide metabolism; Nucleotide-binding; Phosphorylation;
                                                                                                                                                                                                intermediate
                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                  Length 152;
                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mashreghi Mohammadi M.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                            118 118 Pros-phosphohistidine int.
152 AA; 17208 MW; EE2E4DB218024686 CRC64;
                                                                                                                                                                                                                                                                                                      90.8%; Score 729; DB 1;
90.1%; Pred. No. 7.5e-63;
iive 9; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
```

```
TISSUB-Embryonic body between diaphragm region and neck;

WEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

MIkaido I., Osatuo N., Kasukawa T., Adachi J., Bonon H., Kondo S.,

Nikaido I., Osatuo N., Salto R., Suzuki H., Yamanaka I., Kiyosawa H.,

Naja K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

Balake J.A., Bradt D., Prietcher C.F., Forrest A., Frazer K.S.,

Carabold T., Gariboldi M., Gissi C., Godzik A., Frazer K.S.,

Anala B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Grimmond S., Gustincich S., Hirckawa W., Jackson I.J., Jarvis B.D.,

Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konsagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Ravasi T., Reed J.C., Reed D.J., Ring B.Z., Ringwald M.,

Sultana R., Fakenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Num Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

Himing L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,

Num Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

Hirozane-Kishikawa T., Konno H., Nakamura M., Sakzaue N., Sators J.,

Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

M. Mayazaki R., Sakai K., Sasaki D., Sahbata R., Silhada B.,

M. Mayazaki R., Sakai K., Sasaki D., Sahbata R., Silhada B.,

M. Mayazaki R., Sakai K., Sasaki D., Sahbata R., Silhada B.,

M. Mayazaki R., Sakai K., Sasaki D., Sakaki D., Ridade B.S., Rogers J.,

M. Mayazaki R., Sakai K., Sasaki D., Sakaki D., Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J;
TISSUB=Embryonic body between diaphragm region and neck;
TISSUB=Bhoryonic body between diaphragm region and neck;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Peolo G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T., Sakai K., Okido T., Fuzuko M., Tanno H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., dariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodzingez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB=Embryonic body between diaphragm region and neck;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M., Sumin N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M., Yonded Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayabhizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.;
```

```
TISSUB-Embryonic body between diaphragm region and neck;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Rudda S., Furuno M., Hanagaki T., Hara A., Habitaume W.,
Hayashida K., Hayatsu N., Hirancko K., Haracka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Nhazaki R., Ohno M., Ohasto N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogbe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
EMBL, Ak004899; BAC28873.1; -; Genomic_DNA.

BEMBL, Ak004899; BAC28873.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1] -
PROTEIN SEQUENCE, NUCLEOTIDE SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT,
SUBCELLULAR LOCATION, BLOCKAGE OF THE N-TERMINUS, AND X-RAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUJ-1999 (Rel. 38, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Nucleoside diphosphate kinase NBR-B (EC 2.7.4.6) (NDK NBR-B) (NDP kinase NBR-B)
Estaurus (Bovine).
Bustaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovinae; Bosinae;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0005524; F:ATP binding; IEA.
GO:0016301; F:kinase activity; IEA.
GO:00164550; F:nucleoside-diphosphate kinase activity; IEA.
GO:0016740; F:transferase activity; IEA.
GO:0016741; P:CTP biosynthesis; IEA.
GO:001813; P:GTP biosynthesis; IEA.
GO:0006228; P:UTP biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.8%; Score 729; DB 2; Length 152; 90.1%; Pred. No. 7.5e-63; tive 9; Mismatches 6; Indels
sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 AA; 17208 MW; EE2E4DB218024686 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ensembl; ENSMUSG00000037601; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00469; NDP_KINASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PP00334; NDK; 1.
PIRSF; PIRSP00735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
SMART; SM00562; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 90.13
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDKB BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDKB BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    င္ပဲ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

ö

9 9

```
TISSUE=Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                  NDKA BOVIN
P52174;
                                SEQUENCE
                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       removed.
                                                                                      Local
                                                                                                                                           ઠ
                                                                                                                                                                           셤
                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                        요
                                                                                                                                                                                                                                                                                                                                                                                                                    DEPTH TO THE TRANSPORT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE 
                                                                                                                                                                                                                                                                                                                                                                           This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                        Biochemistry 37:11958-13967(1998).
-!- FUNCTION: Major role in the synthesis of nucleoside triphosphates other than ATP.
-!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + nucleoside triphosphate.
-!- COFCTOR: Magnesium (By similarity).
-!- SUBUNIT: Homohexamer.
-!- SUBUNIT: Homohexamer.
                              ABDLINE-98434367; PubMed=9760230; DOI=10.1021/bi9808538; Abdulaev N.G., Karaschuk G.N., Ladner J.E., Kakuev D.L., Yakhyaev A.V., Tordova M., Gaidarov I.O., Popov V.I., Fujiwara J.H., Chinchilla D., Eisenstein E., Gilliland G.L., Ridge K.D.; "Nucleoside diphosphate kinase from bovine retina: purification, subcellular localization, molecular cloning, and three-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pros-phosphohistidine intermediate. Substrate ATP/NDP ribose. Substrate ATP/NDP base. Substrate ATP/NDP beta phosphate. Substrate ATP/NDP beta phosphate. Substrate ATP/NDP beta phosphate. Substrate ATP/NDP base phosphate. Substrate ATP/NDP base. Substrate ATP/NDP pase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
Probom; PD001018; NDK; 1.
SMART; SM00562; NDK; 1.
SMART; SR00469; NDP KINASES; 1.
3D-structure; ATP-binding; Direct protein sequencing; Kinase; Magnesium; Metal-binding; Nuclear protein; Nucleotide metabolism; Nucleotide-binding; Phosphorylation; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Substrate GDP N2
                                                                                                                                                                                                                                                                                                         membrane.
-!- PTM: The N-terminus is blocked.
-!- SIMILARITY: Belongs to the NDK family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X92957; CAA63533.1; -; mENA.
DBB; 1BE4; X-raq. A/B/C=1.151.
InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                444
525
586
60
60
71
71
80
80
95
                                                                                                                                           structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INIT MET
ACT SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                          removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING
BINDING
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
BINDING
BINDING
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HELIX
HELIX
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HELIX
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TURN
HELIX
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HELIX
HELIX
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.CR.N
```

```
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the European Bioinformatics. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                      62 PGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSD 121
                                                                                                                                                                                                                                                                                                                                                                                                                61 AGLVKYWHSGPVVAMVWEGLNVVKTGRVWLGETNPADSKPGTIRGDFCIQVGRNIHGSD 120
                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                2 ANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFF
                                                                                                                                                                                                                                                                                 structure.";
Biochemistry 37:13958-13967(1998).
-!- FUNCTION: Major role in the synthesis of nucleoside triphosphates
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98434367; PubMed=9760230; DOI=10.1021/bi980853s; Abdulaev N.G., Karaschuk G.N., Ladner J.E., Kakuev D.L., Yakhyaev A.V., Tordova M., Gaidarov I.O., Popov V.I., Fujiwara J.H., Chinchilla D., Eisenstein E., Gillilland G.L., Ridge K.D.; "Nucleoside diphosphate kinase from bovine retina: purification, subcellular localization, molecular cloning, and three-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other than ATP.
-!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
nucleoside triphosphate.
-!- CORACTOR: Magnesium (By similarity).
-!- SUBGNIT: Homohexamer.
-!- SUBGNIT: Acmohexamer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleoside diphosphate kinase NBR-A (EC 2.7.4.6) (NDK NBR-A) (NDP kinase NBR-A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN SEQUENCE, NUCLEOTIDE SEQUENCE, CATALYTIC ACTIVITY, ESUBCELLULAR LOCATION, BLOCKAGE OF THE N-TERMINUS, AND X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                        Length 151;
                                                                                                                                                                                   4; Indels
135 137
146 149
151 AA; 17167 MW; AACDC542C77864E1 CRC64;
                                                                                                                     90.7%; Score 728; DB 1;
90.1%; Pred. No. 9.3e-63;
iive 11; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 34, Created)
(Rel. 38, Last sequence update)
(Rel. 47, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 SVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 SVESAEKEIALWFRPEELVNYKSCAQNWIYE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane.
-!- PTM: The N-terminus is blocked.
-!- SIMILARITY: Belongs to the NDK family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X92956; CAA6352.1; -; mRNA.
PDB; 1BHN; X-ray; AB/C/D/E/F=1-151
InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00334; NDK; 1.
PIRSF, PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
                                                                                                                                                                                      Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
```

```
Search completed: December 16, 2005, 16:37:02
Job time : 141.528 Becs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinase
  RATTA DORKT TA DORK TA TA DORK TA TA DORK TA TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK TA DORK T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNI1HGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKRGTIRGDFCIQVGRNIHGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
SMART; SM00562; NDK; 1.
PROSITE: PS00469; NDP KINASES; 1.
3D-structure; AFP-binding; Direct protein sequencing; Kinase;
Magnesium; Metal-binding; Nuclear protein; Nucleotide metabolism;
Nucleotide-binding; Phosphorylation; Transferase.
                                                                                                                                                                                               Substrate ATP/NDP ribose.
Substrate ATP/NDP base.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP base.
Substrate ATP/NDP vibose.
                                                                                                                                                                       Pros-phosphohistidine intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 90.5%; Score 727; DB 1; Length 15
Best Local Similarity 90.1%; Pred. No. 1.2e-62;
Matches 136; Conservative 10; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17130 MW; AAD80B21137EA4E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||:|||||:||| |||||:|||| sesaekeialwyphpeelvnykscaqnwiye 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OSGJV4 BOVIN PRELIMINARY;
QSGJV4;
                                                                                                                                                                       101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NDP kinase NBR-A.
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 :
151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Lymphoid
                                                                                                                                         INIT MET

BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
TURN
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HELIX
STRAND
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HELIX
TURN
TURN
HELIX
TURN
     SO THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE FET THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
```

```
61 FAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIHGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MANLERTFIAIKPDGVQRGLVGBIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Yu J., Meng Y., Wang Z., Hansen C., Li C., Moore S.;
"Analysis of sequences obtained from constructed full-length bovine cDNA libraries.";
Submaitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, AY911378; AAW82141.1; -; mRNA.
                                                                                                                                                                     Ensembl; ENSEMBAG0000004651; Bos taurus.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0004501; F:Rinase activity; IEA.

GO; GO:0004501; F:Rinase activity; IEA.

GO; GO:0006241; F:Cransferase activity; IEA.

R GO; GO:0006241; P:CTP biosynthesis; IEA.

R GO; GO:0006241; P:CTP biosynthesis; IEA.

R GO; GO:0006221; P:CTP biosynthesis; IEA.

R GO; GO:0006222; P:CTP biosynthesis; IEA.

R InterPo; IRR012005; NDK.2.

R PRESPORTATIONS; NDK.1.

R PRESPORTATIONS; NDK; 1.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.3%; Score 725; DB 2; Length 15
89.5%; Pred. No. 1.8e-62;
iive 10; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 AA; 17260 MW; DIDB47DFC731B056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSVKSAEKEISLWFKPEELVDYKSCAHDWVYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00469; NDP_KINASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 89.5%
Matches 136; Conservative
```

This Page Blank (uspto)

```
Q5nc81 m expressed
Q80vt7 mus musculu
Q05982 rattus norv
Q05982 rattus norv
Q65x31 homo sapien
Q5fg31 homo sapien
Q5rc56 pongo pygma
P52175 bos taurus
Q55175 bos taurus
Q56y4 bos taurus
Q56y4 canis famil
Q50ka9 canis famil
Q50ka9 canis famil
Q50ka9 canis famil
Q50ka9 canis famil
Q50ka canis famil
Q50ka canis famil
Q90ria cavia porce
Q5rf13 pongo pygma
Q21392 homo sapien
Q6fh13 homo sapien
Q6fh13 mus musculu
Q6fn2 mus musculu
Q6fn3 catulus gall
Q50r62 mus musculu
Q6fc0 ictalurus p
Q57535 gallus gall
Q9030 columba liv
Q91ad3 brachydanio
Q9030 columba liv
Q91ad3 brachydanio
Q9040 columba liv
Q90101 xenopus lae
Q5073 xenopus lae
Q5073 xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P15532 mus musculu
                                                                                     ; Search time 153.472 Seconds (without alignments) 763.122 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                     876
1 QSQPAVKPCHLKGTWANSER........WFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                            2166443 seqs, 705528306 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDKA, HŪMAN

GERGZI, HUMAN

GERGZI, HUMAN

NDKA, BOVIN

NDKB, BOVIN

NDKA, CANPA

GSGJZ, BONIN

GSGJZ, BONIN

GSGTRA

GSBRTA

NDKB, HÜMAN

GERTÄJ

NDKB, HÜMAN

NDKB, HÜMAN

NDKB, HÜMAN

NDKB, HÜMAN

NDKB, MÜMBN

NDKB, MÜMBN

NDKB, MÜMBN

NDKB, MÜMBN

NDKB, MÜMBN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDK COLLI
Q91AD3 BRARE
Q7SXG5-BRARE
Q9PTF5-BRARE
NDKA2_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q80VT7_MOUSE
NDKA_RAT
Q86XQ2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSNC82 MOUSE
Q9DFC0 ICTPU
O57535 CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q5PQ80 XENLA P70071 XENLA Q6AZK9 XENTR NDKA1 XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                        December 16, 2005, 16:31:58
                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                  UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
                                                                                                                                                    US-10-074-694-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. , Score
                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
```

Q68117 xenopus lae Q86470 oncorhynchu P27950 ginglymchu D27950 salmo salar Q5768 salmo salar Q5768 mus musculu Q78414 brachydanio Q6031 homo sapien Q72247 oreochromis P08879 drosophila Q64711 drosophila Q6471 drosophila Q9ptf3 brachydanio Q9ptf4 brachydanio Q9ptf4 brachydanio		(NDK A) (NDP kinase A) (Metastasis inhibition	A) (nm23-M1). =Nm23;). Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murinae; Mus.	42177a0; 3 J.R., Barker E., 3 P.S.; and aberrant Drosophila	Thorgeirsson U.P., .i with low tumor metastatic).	NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. MEDLINE=91191558; PubMed=2013093; DOI=10.1016/0092-8674(91)90404-M; Leone A., Flatow U., King C.R., Sandeen M.A., Margulies I.M., Liotte L.A., Steeg P.S.; "Reduced tumor incidence, metastatic potential, and cytokine responsiveness of mu23-transfected melanoma cells.";	nBank/DDBJ databages. D.; nBank/DDBJ databages. NAJ.
0668T7 XENLA 0804Y0_ONCMY NDK GINCI 097560 SALSA 05NC80_MOUSE 05NC80_MOUSE 07SX14_BRARE NDK8_HÜMAN 07ZZÖ7 OREMO NDKA_DROME NDKA_DROME 09PTF3 BRARE 09PTF3 BRARE	ALIGNMENTS	152 AA. e update) ion update) con update) ed protein)	M1). ; Craniata; Vertebr toglires; Glires; R Mus.	NUCLECTIDE SEQUENCE. MEDINE=90044071; PubMed=2509941; DOI=10.1038/342177a0; Rosengard A.M., Krutzsch H.C., Shearn A., Biggs J.R., Barker Margulies I.M.K., King C.R., Liotta L.A., Steeg P.S.; "Reduced Nm23/Awd protein in tumour metastasis and aberrant development."; Nature 342:177-180(1989).	UCLECATIDE SEQUENCE. MEDLINE=88155671; PubMed=3346912; Steeg P.S., Bevilacqua G., Kopper L., Thorgeirsson U.P Talmadge J.E., Liotta L.A., Sobel M.E.; "Evidence for a novel gene associated with low tumor m potential."; J. Natl. Cancer Inst. 80:200-204(1988).	3093; DOI=10.1016/0 R., Sandeen M.A., M tastatic potential, fected melanoma cel	141 STRAIN=129/Sv; Dabernat S., Masse K., Daniel J.Y.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ d GETRAIN=Swiss Webster / NIH; Gervasi F., Fanciulli M., Lombardi D.; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ d [6] STRAIN=FVBJN; TISSUE=ARGE SCALE MRNA]. STRAIN=FVBJN; TISSUE=Ammary 91and; STRAIN=FVBJN; TISSUE=Ammary 91and;
00000000000000		eate st s st a st as	m23- ; data data chon ae;	=250 H.C .R., n in	=334 ., k A., ne a	=201 9 C. rans	Daniel the El NIH; the El Company RGE SC
154 151 151 152 153 152 152 156 158		STANDARD; 1. 14, Cr. 1. 14, La. 1. 48, La osphate k ic proces	(-A) (n) ns=Nm23 se). t; Chor n; Euar	De. PubMed Tutzsch King C protei	DubMed PubMed acqua G otta L. ovel ge	DubMed PubMed J., Kin J.P.S.; Sidence nm23-t	CE. (CE.) D 97) to 97) to 12E. / N Long 1311 M. O 97) to 25 [LAR SUE=Mam
78.0 76.0 76.0 77.1 71.1 71.1 71.1 71.1 71.1 71.1 71		ST? (Rel. (Rel. (Rel. (Rel. diphosi) (NDPP Synonyn B (Mout Metazos utheria uridae;	SEQUENC 44071; .M., Ki .M.K., 23/Awd .";	SEQUENC 55671; Bevila E., Lic or a nc	SEQUENC 91558; latow U , Stees mor inc ess of 35(1993	SEQUENCE /8v; ., Masse (FEB-1997 SEQUENCE se Webste; , Fanciul (NOV-1997 /N; TISSU
688 6666 6670 6688 6688 6688 670 6888 6888		ULT 1 A_MOUSE STANDARD; PRT; P15532; 01-APR-1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last sequenc) 13-SEP-2005 (Rel. 48, Last annotat) Nucleoside diphosphate kinase A. (Tumor metastatic process-associate	factor NM3) (NDPK-A) (nm23-M1) Name-Nmel; Synonyme-Nm23; Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; C Mammalia; Eutheria; Euarchontog Muroidea; Muridae; Murinae; Mus NCEI_TaxID=10090;	NUCLEOTIDE SEQUENCE. MEDLINE-90044071; Pu Rosengard A.M., Krut marquilee I.M.K., Ki "Reduced Nm29/Awd px development.";	NULBOTIDE SEQUE MEDLINE=88155671 Steeg P.S., Bevi Talmadge J.E., I "Evidence for a potential.";	LECTIDE LINE=911 me A., F tta L.A. duced tu ponsiven 1 65:25-	14) STRAIN=129/Sv; Dabernat S., Masse K., Daniel J.Y.; Dabernat (FEB-1997) to the EMBL/Ge [5] NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE (GETVABLE) Submitted (NOV-1997) to the EMBL/Ge [6] NUCLEOTIDE SEQUENCE (LARGE SCALE MR STRAIN=FWABN) STRAIN=FWABN TISSUE-MARMMARY GLANGE STRAIN=FWABN TISSUE-MARMMARY GLANGE STRAIN=FWABN TISSUE-MARMMARY GLANGE STRAIN=FWABN TISSUE-MARMMARY GLANGE STRAIN=FWABN TISSUE-MARMMARY GLANGE STRAIN—FWABN TISSUE-MARMARY GLANGE STRA
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~		RESULT 1 NDKA_MOUSE ID NDKA_A AC 01-5557 DT 01-4PF DT 01-APF DT 13-SE DE (Autle)	Facto Name: Mus r Bukar Mamm: Muro	[1] NUC NUC ROS ROS MAR "Re dev	MED MED Ste Tal	[3] NUC NUC Leo Lio Res Res Cel	STR STR SUD SUD SUD STR SER SUD SUD SUD SUD SUD SUD SUD SUD SUD SUD

ò

1 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF 60 PRT; sequence). ORFNames=RP23-378I13.1-001; QSNC81 MOUSE PRELIMINARY; Nature 409:685-690(2001) NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE NCBI_TaxID=10090; Hayashizaki Y.; MOUSE Q5NC81; RESULT Q5NC81 ò 셤 ઠ Atlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soarsea M.B., Bonaldo M.F., Carahni T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tooshiyuki S., Carahni P.L., Fange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Broak S.A., McEwan P.J., McKernan K.J., Make J.A., Guay L.J., Hulyk S.W., Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton B., Ketreman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Butkerfield Y.S.N., Krzywinski M.I., Skalaka U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.N., Marra M.A., Schein J.E., Jones S.J.N., Marra M.A., Schein J.E., Jones S.J.N., Marra M.A., Shenerch A., Schein J.E., Jones S.J.N., Marra M.A., Shenerch A., Schein J.E., Jones S.J.N., Marra M.A., Shenerch A., Schein J.E., Jones B.J.N., Marra M.A., Shenerch A., Schein J.E., Jones B.J.N., Marra M.A., Shenerch A., Schein J.E., Jones Han 15,000 full-length human and washed and the second and statement and the second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and second and sec This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not ö nucleoside triphosphate.
-!- COFACTOR: Magnesium (By similarity).
-!- TOFACTOR: Magnesium (By similarity).
-!- SUBUNIT: Hexamer of two different chains: A and B (A6, A5B, A4B2, A3B3, A2B4, A8B, B6). Interacts with SET (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
-!- DISEASE: This protein is found in reduced amount in tumor cells of and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- FUNCTION: Major role in the synthesis of nucleoside triphosphates other than ATP. The ATP gamma phosphate is transferred to the NDP beta phosphate via a ping-pong mechanism, using a phosphorylated cotive-site intermediate.
-!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP + PROSITE; PS00469; NDP KINASES; 1. ATP-binding; Kinase; Magnesium; Metal-binding; Nuclear protein; 118 118 Pros-phosphohistidine intermediate. 152 AA; 17208 MW; EE2E4DB218024686 CRC64; ö 91.1%; Score 798; DB 1; Length 152; ilarity 100.0%; Pred. No. 6.5e-67; Conservative 0; Mismatches 0; Indels Nucleotide metabolism; Nucleotide-binding; Phosphorylation -1- SIMILARITY: Belongs to the NDK family. SMR; P15532; 5-152.
SWISS-2DPAGE; P15532; MOUSE.
Ensembl; ENSMUSG00000037601; Mus musculus.
MGI; MGI:97355; Nme1.
GO:0005792; C:md.crosome; IDA.
GO: GO:0005792; C:md.crosome; IDA. EMBL; M35970; AAA39826.1; ALT INIT; mRNA. EMBL; M65037; AAA63391.1; -; mRNA. EMBL; U85511; AAB42080.1; -; mRNA. EMBL; AF033377; AAB87689.1; -; mRNA. EMBL; BC005629; AAH05629.1; -; mRNA. Pfam, PF00334, NDK, 1.
PIRSF, PIRSF000735, NDK, 1.
PRINTS, PR01243, NUCDPKINASE.
PRODOM; PD001018, NDK, 1. high metastasic potential InterPro; IPR001564; NDK. InterPro; IPR012005; NDK-2. PIR; A46557; A46557. HSSP; P15531; 1JXV. NDK; Similarity SM00562; ransferase. Best Local Sim: Matches 152; Query Match removed. SMART;

```
STRAIN-CSTBL/GS.

CSTRAIN-CSTBL/GS.

CSTRAIN-CSTBL/GS.

TISSUB-Embryonic body between diaphragm region and neck;

TISSUB-Embryonic body between diaphragm region and neck;

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Pukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Rachota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schrim I., M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,

Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Ring B., Ringwald K.H., Weitz C., Whittaker C., Wilming L.,

Nordone P., Rodriguez C., Schoenbach C., Seya T., Shibata Y., Kohtsuki S.,

Nordone P., Rodriguez C., Schoenbach C., Seya T., Shibata Y., Kawaji H., Kohtsuki S.,

Nordone P., Rodriguez C., Schoenbach C., Seya T., Shibata Y., Kawaji H., Kohtsuki S.,

Nordone P., Kohtsuki S.,
                            61 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
75 FIGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                                 01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Expressed in non-metastatic cells 1 protein (12 days embryonic body between diaphragm region and neck CDNA, RIKEN full-length enriched library, clone:9430059B17 product:expressed in non-metastatic cells 1, protein (NM23A) (nucleoside diphosphate kinase), full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS7BL/6J;
TISSUB=Embryonic body between diaphragm region and neck;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
Hidh-efficiency full-length cDNA cloning.";
Midh-efficiency full-1ength cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .... muscurse procest.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Embryonic body between diaphragm region and neck;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
ORazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mashreghi-Mohammadi M.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                            135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                         121 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                         152 AA.
```

```
Kinase
                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Ra Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Ra Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Balae J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Ra Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Marchionni L., McKenzie L., Miki H., Ra Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Ra Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Ra Maglott D.R., Marchioni L., Marchada B., Lyons P.A., Ragashima T., Numata K., Okido T., Pavan W.J., Pertea G., Peole G., Reed D.J., Reid J., Ring B.Z., Ringaald M., Reded J.C., Reed D.J., Reid J., Ring B.Z., Ringaald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Walming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I., Yang I., Yang I., Yang I., Yang I., Aninning L.G., Wynshaw-Boris A., Yanagisawa M., Zardawa T., Ronno H., Nakamura M., Sakazume N., Sakai K., Sasaki D., Shibata K., Shinagawa A., Hashizume W., Imotani J., Aizawa K., Arakawa T., Rukuda S., Ayasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Ranalysis of the mouse transcriptome based on functional annotation of K. Marry A., Analysis of the mouse transcriptome based on functional annotation of M. Marry A., A., Kanama M., Kalawa I., Marry A., A., Kalawa I., Marry A., Kalawa I., Marry A., Kalawa I., Marry A., A., Kalawa I., Marry A., A., Kalawa I., Marry A., A., Kalawa I., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C STRAIN-CSTBL/GS:

C TISSUE-Embryonic body between diaphragm region and neck;

Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

Hayashida K., Ishii Y., Itoh M., Kagawa T., Kaukawa T.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Kurihara C., Matsuyama T., Myazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

Saito R., Saitoh H., Sakai C., Sakai K., Sakazuwa N., Sakazuwa D., Shinada K., Shinaqawa A., Sakazuwa N., Sakazuwa A., Tagami M.,

Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasuuishi A., Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL, AKO34899; BAC28873.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CS7BL/6J;

STRAIN=CS7BL/6J;

TISSUB=Embryonic body between diaphragm region and neck;

MEDLINE=20499374; PubMed=11042159; DoI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

Wornalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes.";

Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=2,000,001,
MEDLINE=20530913, PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Riki integrated sequence analysis (RISA) system-384-format
Sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J;
```

musculus.

Ensembl; ENSMUSG00000037601; Mus mv GO; GO:0005524; F:ATP binding; IEA

```
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Antschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
C. Garmeration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FTGLVKYM4SGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0004500; F:nucleoside-diphosphate kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006241; P:CTP biosynthesis; IEA.
GO; GO:0006228; P:CTP biosynthesis; IEA.
InterPro; IPR001564; NDK.
InterPro; IPR0012664; NDK.
Pfam; PF00314; NDK: 1.
PIRSF; PIRSF000735; NDK: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.1%; Score 798; DB 2; Length 152; 100.0%; Pred. No. 6.5e-67; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 AA; 17208 MW; EE2E4DB218024686 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 176 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00469; NDP_KINASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01243; NUCDPKINASE.
SMART; SM00562; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OBOVI7 MOUSE PRELIMINARY;
Q80VI7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nm23 protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissum=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPARANCE OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING TO THE PROPERTY OCCOORDING
```

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
Q86XQ2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NM23-H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Мао У
SO TIME AND DESCRIPTION OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 KEHYTDLKDRPFFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLECTIDE SEQUENCE.
MEDLINE=93155067; PubMed=8381409;
Shimada N., Ishikawa N., Munakata Y., Toda T., Watanabe K., Kimura N.;
A second form (beta isoform) of nucleoside diphosphate kinase from rat. Isolation and characterization of complementary and genomic DNA and expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 QPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 KEHYVDLKDRPFPAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF

    Biol. Chem. 268:2583-2589(1993).
    FUNCTION: Major role in the synthesis of nucleoside triphosphates other than ATP. The ATP gamma phosphate is transferred to the NDP beta phosphate via a ping-pong mechanism, using a phosphorylated active-site intermediate.
    CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
11-SEP-2005 (Rel. 48, Last annotation update)
Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase A)
(Tumor metastatic process-associated protein) (Metastasis inhibition factor NM23).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                          Ensembl; C880VT7; 28-176.
Ensembl; ENSWUSG00000037601; Mus musculus.
GO; GO:0005501; F.ATP binding; IEA.
GO; GO:0016501; F.Ininse activity; IEA.
GO; GO:0016740; F.Inucleoside-diphosphate kinase activity; IEA.
GO; GO:0006241; P:CTP biosynthesis; IEA.
GO; GO:0006281; P:CTP biosynthesis; IEA.
GO; GO:00062828; P:UTP biosynthesis; IEA.
                           Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER 1 1 1 SEQUENCE 176 AA; 19979 MW; 27C36B3DB3F895E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE, PS00469, NDP KINASES, 1.
ATP-binding, Kinase, Nucleotide-binding, Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.6%; Score 794; DB 2;
91.5%; Pred. No. 1.8e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 AA
                                                                                          nucleoside triphosphate.
-!- SIMILARITY: Belongs to the NDK family.
EMBL; BC027044; AAH27044.2; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pfam; PF00334; NDK; 1.
PRINTS; PROLE43; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
SWART; SMO0562; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleoside triphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001564; NDK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity ... Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                  P15531; 1JXV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Nme1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
Service Reservation of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

```
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FSGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
-!- COFACTOR: Magnesium (By similarity).
-!- SUBUNIT: Hexamer of two different chains: A and B (A6, A5B, A4B2, A33, A2B4, AB5, B6). Interacts with SET (By similarity).
-!- SUBCELLULAR LOCATION: Unclear and cytoplasmic.
-!- DISEASE: This protein is found in reduced amount in tumor cells of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFIQASEDLLKEHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               자.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
MEDLINE=22489419; PubMed=12601555; DOI=10.1007/s100380300014;
Ni X., Gu S., Dai J., Cheng H., Guo L., Li L., Ji C., Xie Y., Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Isolation and characterization of a novel human NM23-H1B gene, different transcript of NM23-H1."; J. Hum. Genet. 48:96-100(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 779; DB 1; Length 152;
Pred. No. 4e-65;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32C49E6271195C3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P15531; 1JXV.
SMR; Q05982; 5-152.
Ensembl; ENSRNOG0000002693; Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 DSVESAEKEISLWFQPEELVDYKSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 AA
                                                                                                                                                  high metastasic potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D13374; BAA02635.1; -; mRNA.
PIR; A45208; A45208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGD; 70497; Nmel.
Cocontrosome; IDA.
InterPro; IPR01564; NDK-2.
InterPro; IPR012005; NDK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 AA; 17193 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEAM; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 96.7%;
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q86XQ2;
01-JUN-2003 (TEMBLrel. 24,
01-JUN-2003 (TEMBLrel. 24,
01-OCT-2003 (TEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q86XQ2_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00562; NDK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
```

SO DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESERVA DE RESER

```
TISSUB-Brain, and Lung;

WEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RIJAUBRER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RIJAUBRER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Parter A.A., Rubin G.M., Heiseh F.,

Diatchenko L., Marusina K., Parter A.A., Rubin G.M., Hong L.,

Rab S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

N. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rabesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Bulkerifield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIANE=22853468; PubMed=12972261; DOI=10.1016/j.jmb.2003.07.004; Chen Y., Gallois-Montbrun S., Schneider B., Veron M., Morera S., Deville-Bonne D., Janin J.; "Nucleotide binding to nucleoside diphosphate kinases: X-ray structure of human NDPK-A in complex with ADP and comparison to protein
Wang L., Patel U., Ghosh L., Chen H.C., Banerjee S.;
"Mutation in the nm23 gene is associated with metastasis in colorectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE OF 7-18; 40-49 AND 89-94, AND DISEASE.
MEDLINE=91277302; PubMed=2056128;
Hailat N., Keim D.R., Melhem R.F., Zhu X.X., Eckerskorn C.,
Brodeur G.M., Reynolds C.P., Seeger R.C., Lottspeich F.,
Strahler J.R., Hanash S.J.,
"High levels of p19/nm23 protein in neuroblastoma are associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99443867; PubMed=10512675; DOI=10.1006/geno.1999.5939; Manda R., Kohno T., Mateuno Y., Takenoshita S., Kuwano H., Yokota J.; Aldentification of genes (SPONZ and C20orf2) differentially expressed between cancerous and noncancerous lung cells by mRNA differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22515524; PubMed=12628186; DOI=10.1016/S0092-8674(03)00150-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND MUTAGENESIS OF PHE-60 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gilles A.-M., Presecan E., Vonica A., Lascu I., "Nucleoside diphosphate kinase from human erythrocytes. Structural characterization of the two polypeptide chains responsible for hererogeneity of the haxameric enzyme."; J. Biol. Chem. 266:8784-8789(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDILINE=21824372; PubMed=1183569; DOI=10.1002/prot.10038;
Min K., Song H.K., Chang C., Kim S.Y., Lee K.J., Suh S.W.;
"Crystal structure of human nucleoside diphosphate kinase A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   advanced stage disease and with N-myc gene amplification."; J. Clin. Invest. 88:341-345(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN SEQUENCE, SUBUNITS, AND ACTIVE SITE.
MEDLINE=91224972; Pubmed=1851158;
                                                                                                                                                  SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Biol. 332:915-926(2003)
                                                                                     Cancer Res. 53:717-720(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metastasis suppressor.";
Proteins 46:340-342(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 61:5-14(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH SET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FISSUE SPECIFICITY.
                                                                                                                                                  NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           display.
         64 EHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
MEDLINE=90044071; PubMed=2509941; DOI=10.1038/342177a0;
Rosengard A.M., Krutzsch H.C., Shearn A., Biggs J.R., Barker E.,
Margulies I.M.K., King C.R., Liotta L.A., Steeg P.S.;
"Reduced Nm23/Awd protein in tumour metastasis and aberrant Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 PAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation and characterization of the human genomic locus coding for the putative metastasis control gene nm23-H1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
13-SPB-2005 (Rel. 48, Last annotation update)
Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase A)
(Tumor metastatic process-associated protein) (Metastasis inhibition factor nm23) (nm23-H1) (Granzyme A-activated DNase) (GAAD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94095204; PubMed=8270257; DOI=10.1007/BF00218915; Dooley S., Seib T., Engel M., Theisinger B., Janz H., Piontek K., Zang K.D., Welter C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                    GO:0005524; F:ATP binding; IEA.
GO:0016301; F:ATP binding; IEA.
GO:0016301; F:Kinase activity; IEA.
GO:0004550; F:nucleoside-diphosphate kinase activity; IEA.
GO:0016740; F:transferase activity; IEA.
GO:0006741; P:CTP biosynthesis; IEA.
GO:0006183; P:CTP biosynthesis; IEA.
GO:0006228; P:UTP biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.4%; Score 774.5; DB 2; Length 177; 90.2%; Pred. No. 1.3e-64; ive 4; Mismatches 11; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 IQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQVGRNIIHGSDSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 AA; 19654 MW; DEA9961E992D0378 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 AA
                                                                                           Ensembl; ENSG0000011052; Homo sapiens.
      EMBL; AF487339; AAO85436.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                 PERM; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
SMART; SM00562; NDK; 1.
PROSITE; PS00469; NDP KINASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
MEDLINE=93153759; PubMed=7916650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=NME1; Synonyms=NDPKA, NM23;
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genet, 93:63-66(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 90.2
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 342:177-180(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDKA HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
```

P15531

RESULT 6 NDKA_HUMAN

g

ઠ 원 ò 셤

ò

```
RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q6FGK3
        DAT THE POLICE OF THE PROPERTY OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE OF THE POLICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMHL outstation the European Bioinformatics. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fan Z., Beresford P.J., Oh D.Y., Zhang D., Lieberman J.; "Tumor suppressor NM23-H1 is a granzyme A-activated DNase during CTL-mediated apoptosis, and the nucleosome assembly protein SET is its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Major role in the synthesis of nucleoside triphosphates
                                                                                                                                                                                                                                VARIANT NEUROBLASTOMA GLY-120.
MEDLINE=94322908; PubMed=8047138; DOI=10.1038/370335a0;
Chang C.L., Zhu X.-X., Thoraval D.H., Ungar D., Rawwas J., Hora N. Strahler J.R., Hanash S.M.;
"Nm23-H1 mutation in neuroblastoma.";
Nature 370:335-336(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005634; C:nucleus; NAS.
GO; GO:0005524; F:ATP binding; NAS.
GO; GO:0004536; F:deoxyribonuclease activity; IDA.
GO; GO:0003677; F:DRA binding; IC.
GO; GO:0004550; F:magnesium ion binding; IDA.
GO; GO:0004550; F:nucleoside-diphosphate kinase activity; NAS.
GO; GO:0008285; P:nucleoside triphosphate biosynthesis; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART, SMOGSEZ, ND. 1... PROSTTE; SMOGSEZ, ND. PROSTTE; PSOG469; NDP KINASES; 1. BROSTTE; PSOG469; NDP KINASES; 1. BROSTTE; PSOG469; NDP KINASES; 1. Direct protein sequencing; Disease mutation; Kinase; Magnesium; Metal-binding; Nuclear protein; Nucleotide metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other than ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the NDK family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X17620; CAA35621.1; ALT INIT; MRNA.
EMBL; X75598; CAA53270.1; -; Genomic_DNA.
EMBL; X73066; CAA51527.1; -; MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PMMA-2DPAGE; P15531; -.
Ensembl; ENSG00000111052; Homo sapiens.
HGNC; HGNC; 7849; NME1.
H-InvDB; HIX0013992; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, BC000293; AAH00293.1; -; mRNA. BMBL; BC018994; AAH18994.1; -; mRNA. PTR, A3386. A3386. PDB; 1JXV, X-ray; A/B/CD/E/F=1-152. PDB; 1UXV; X-ray; A/B/C=1-152. Aarhus/Ghent-2DPAGE; 4115; IEF. Aarhus/Ghent-2DPAGE; 5112; IEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEam; PP00334; NDK; 1.
PIRSF, PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCDPKINASE.
ProDom; PD001018; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleoside triphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
                                                                                                                                                            Cell 112:659-672(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reactome; P15531; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OGP; P15531; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 removed.
        \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z} \mathcal{Z}
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 FAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                      74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MANCERTFIAIKPDGVQRGLVGEIIKRFEQXGFRLVGLKFWQASEDLLKEHYVDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                      15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                              S -> G (in neuroblastoma).
/FTId=VAR 004625.
F->W: No loss of activity or substrate
                                         Substrate ATP/NDP base.
Substrate ATP/NDP base.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP base.
Substrate ATP/NDP base.
Substrate ATP/NDP ribose.
               Pros-phosphohistidine intermediate.
                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ensembl; ENGCOLOGO11052; Homo sapiens.

GO; GO: 0005524; F:ATP binding; IEA.

GO; GO: 0016301; F:Kinase activity; IEA.

GO; GO: 0016450; F:transferase activity; IEA.

GO; GO: 000641; P:CTP biosynthesis; IEA.

GO; GO: 000621; P:CTP biosynthesis; IEA.

GO; GO: 0006228; P:UTP biosynthesis; IEA.

HATEPER; IPRO12605; NDK.-2.

PEAM; PF00334; NDK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S., Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W. Korn B., Zuo D., Hu Y., LaBaer J.; Submitted D., Hu Y., LaBaer J.; Submitted CR542104; Code46901.; -; mRNA. EMBL, CR542115; CAG46901.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                   86.6%; Score 759; DB 1; Length 152; 94.1%; Pred. No. 3e-63;
                                                                                                                                                                                                                                                                                                                                                                                                    6; Indels
                               Substrate ATP/NDP ribose.
                                                                                                                                                                                                                                  H->G: Loss of activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
Phosphorylation; Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 DSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z
                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152
                                                                                                                                                                                                                   binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 10-MAX-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEFGK3 HUMAN PRELIMINARY;
QEFGK3;
                                                                                                                                                                                                                                                                                                                                                                                                      Matches 143; Conservative
               118
60
60
88
94
105
1112
1115
120
                                                                                                                                                                                                                                118
111
17
17
19
31
31
                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
Nucleotide-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q6FGK3; 4-152.
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                 118
60
88
88
112
112
112
112
113
120
                                                                                                                                                                                                                                                    6
113
118
32
34
                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NME1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=NME1;
               ACT SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                             BINDING
BINDING
BINDING
BINDING
                                                                                                                               BINDING
BINDING
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                        Best Local
                                                                                                                                                                                                   MUTAGEN
                                                                                                                                                                                                                                  MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                                               BINDING
                                                                                                                                                                                                                                                  STRAND
                                                                                                                                                                                                                                                                                                                                      STRAND
                                                                                                                                                                                                                                                                                   TURN
HELIX
                                                                                                                                                                                                                                                                                                                    TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMR;
```

_

```
MEDLINE=98434367; PubMed=9760230; DOI=10.1021/bi9808538;
                                                               DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                         121 DSVESAEKEIGLWFHPEELVDYTSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: The N-terminus is blocked.
-!- SIMILARITY: Belongs to the NDK family.
                                                                                                                                                                                                              151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X92956; CAA63532.1; -; mRNA.
PDB; 1BHN; X-ray; AB/C/D/E/F=1-151.
InterPro; IPR01264; NDK-2.
InterPro; IPR012005; NDK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochemistry 37:13958-13967(1998)
                                                                                                                                                                                                                                                                                                                                                                                                               Pecora; Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01243; NUCDPKINASE. ProDom; PD001018; NDK; 1. SMART; SM00562; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111
111
59
87
93
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structure.";
                                                                                                                                                                                                              BOVIN
                                                                 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INIT MET
ACT SITE
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           removed
                                                                                                                                                                                                                               8
                                                                                                   셤
                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                    61 FAGLVKYMHSGPVVAMVWEGLAVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                            75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                              74
                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukāryotā, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFWQASEDLLKEHYVDLKDRPF
                                                                                                                                                                                                            15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                     .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016301; F:Kinase activity; IEA.
GO; GO:0016301; F:Kinase activity; IEA.
GO; GO:0004550; F:nucleoside-diphosphate kinase activity; IEA.
GO; GO:0006241; P:CTP biosynthesis; IEA.
GO; GO:0006218; P:GTP biosynthesis; IEA.
GO; GO:0006228; P:GTP biosynthesis; IEA.
InterPro; IPR001564; NDK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 759; DB 2; Length 152;
Pred. No. 3e-63;
                                                                                                                           Score 759; DB 2; Length 152;
Pred. No. 3e-63;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. –
SEQUENCE 152 AA; 17149 MW; AAE9CODF63CB70A1 CRC64;
                                                               PROSITE; PS00469; NDP KINASES; 1.
SEQUENCE 152 AA; 17149 MW; AAE9CODF63CB70A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein DKFZp46800911.
                                                                                                                                                                                                                                                                                                                                                                             135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                  |||:|||||| ||| ||| ||||:| ||||||||
DSVESAEKEIGLWFHPEELVDYTSCAONNIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00469; NDP_KINASES; 1.
                           PR01243; NUCDPKINASE. SM00562; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01243; NUCDPKINASE, ProDom; PD001018; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.6%;
                                                                                                                             86.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.18;
                                                                                                                                                  94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR012005; NDK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pongo pygmaeus (Orangutan).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
        PIRSF; PIRSF000735; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSRC56_PONPY PRELIMINARY;
QSRC56;
                                                                                                                                                    Best Local Similarity 94.1
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM00562; NDK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4-152.
                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMR; 05RC56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rissum=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro
                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PONPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAT DATE OF THE PROPERTY OF THE PARTY OF THE
          88888
88888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                    임
                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

```
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: Major role in the synthesis of nucleoside triphosphates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abdulaev N.G., Karaschuk G.N., Ladner J.E., Kakuev D.L., Yakhyaev A.V., Tordova M., Galdarov I.O., Popov V.I., Fujiwara J.H., Chinchilla D., Eisenstein E., Gilliland G.L., Ridge K.D., "Nucleoside diphosphate Kinase Erom bovine retina: purification, subcellular localization, molecular cloning, and three-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT
01-0CT-1996 (Rel. 34, Created)
15-UTL-1999 (Rel. 38, Last sequence update)
16-UTL-1999 (Rel. 47, Last annotation update)
Nucleoside diphosphate kinase NBR-A (EC 2.7.4.6) (NDK NBR-A) (NDP kinase NBR-A)
                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other than ATP.
-!- CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP +
nucleoside triphosphate.
-!- COFACTOR: Magnesium (By similarity).
-!- SUBUNIT: Homohexamer.
-!- SUBCELLULAR LOCATION: Cytoplasmic and localized to the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00469; NDP KINASES; 1.
Distructure; AFP-binding; Direct protein sequencing; Kinase;
Magnesium; Metal-binding; Nuclear protein; Nucleotide metabolism;
Nucleotide-binding; Phosphorylation; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pros-phosphohistidine intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Substrate ATP/NDP ribose.
Substrate ATP/NDP base.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP beta phosphate.
Substrate ATP/NDP base.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN SEQUENCE, NUCLEOTIDE SEQUENCE, CATALYTIC ACTIVITY, & SUBCELLULAR LOCATION, BLOCKAGE OF THE N-TERMINUS, AND X-RAY CRYSTALLOGRAPHY (2.4 ANGSIROMS).
```

TELIX

TURN

```
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 ANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E BMBL; X92957; CAA63533.1; -; mRNA.

R InterPro; IPR001564; NDK.

R InterPro; IPR001564; NDK-2.

R PIRSF; PIRSF000735; NDK-1.

R PIRSF; PIRSF000735; NDK; 1.

R PRINST; PR00143; NUCDFKINASE.

R PROSTTE; PR00162; NDK; 1.

R PROSTTE; PR00469; NDK; 1.

R PROSTTE; PR00469; NDK; 1.

M 3D-structure; ATP-binding; Direct protein sequencing; Kinase; M Adgresium; Metal-binding; Nuclear protein; Nucleotide metabolism; Nucleotide-binding; Phosphorylation; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                     to the plasma
                                                                                                                                                                                                                                                                                                                                                                         Pros-phosphohistidine intermediate
                                                                                                                                                                                                                                                                                                                                                                                                 base.
beta phosphate.
beta phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        beta phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.5%; Score 749; DB 1; Length 151; larity 92.7%; Pred. No. 2.6e-62; Conservative 7; Mismatches 4; Indels
  CATALYTIC ACTIVITY: ATP + nucleoside diphosphate = ADP
                                                                                                                                                                                                                                                                                                                                                                                   Substrate ATP/NDP ribose.
Substrate ATP/NDP base.
Substrate ATP/NDP beta phost
Substrate ATP/NDP beta phost
Substrate ATP/NDP beta phost
Substrate ATP/NDP base.
Substrate ATP/NDP base.
Substrate ATP/NDP vibose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17167 MW; AACDC542C77864E1 CRC64;
                         COFACTOR: Magnesium (By similarity).
SUBUNIT: Homohexamer.
SUBCELLULAR LOCATION: Cytoplasmic and localized
                                                                           PTM: The N-terminus is blocked. SIMILARITY: Belongs to the NDK family.
               nucleoside triphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
33
33
33
52
53
63
63
63
80
80
                                                                  membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Sim:
Matches 140;
                                                                                                                                                                                                                                                                                                                                                            ACT SITE
ACT SITE
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                    removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAND
HELIX
TURN
HELIX
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAND
HELIX
HELIX
TURN
HELIX
HELIX
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HELIX
STRAND
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HELIX
HELIX
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TURN
   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                     135
                                                                                                                                                                                                                                                                                                                                                                                                   75
                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGSD
                                                                                                                                                                                                                                                                                                                                                                                                   16 ANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPFF
                                                                                                                                                                                                                                                                                                                                                                                                                  1 ANSERTFIAIKPDGVQRGLIGEIIKRFEQKGFRLVAMKFMRASEDLLKEHYIDLKDRPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochemistry 37:13958-13967(1998).
-1- FUNCTION: Major role in the synthesis of nucleoside triphosphates other than ATP.
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Retina;
MEDLINE=98434367; PubMed=9760230; DOI=10.1021/bi980853s;
Abdulaev N.G., Karaschuk G.N., Ladner J.E., Kakuev D.L.,
Yakhyaev A.V., Tordova M., Gaidarov I.O., Popov V.I., Fujiwara J.H.
Chinchilla D., Eisenstein E., Gilliland G.L., Ridge K.D.;
"Nucleoside diphosphate kinase from bovine retina: purification, subcellular localization, molecular cloning, and three-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE, NUCLEOTIDE SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, BLOCKAGE OF THE N-TERMINUS, AND X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
15-UU-1999 (Rel. 38, Last sequence update)
16-UU-1999 (Rel. 47, Last annotation update)
Nucleoside diphosphate kinase NBR-B (EC 2.7.4.6) (NDK NBR-B) (NDP kinase NBR-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                  Length 151;
                                                                                                                                                                                                                                                                                                                                              85.6%; Score 750; DB 1; Length 15
92.7%; Pred. No. 2.1e-62;
ive 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                       17130 MW; AAD80B21137EA4E1 CRC64;
 Substrate ATP/NDP ribose. Substrate GDP N2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 SVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 AA
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 92.7
Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
   structure.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDKB BOVIN
P52175;
                                                                                                                                                                                                                                                                                                          HELIX
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
BINDING
BINDING
STRAND
HELIX
TURN
                                                                          TURN
STRAND
HELIX
HELIX
TURN
TURN
HELIX
STRAND
TURN
                                                                                                                                                                                                                  TURN
HELIX
TURN
STRAND
HELIX
HELIX
```

RESULT 10 NDKB_BOVIN

셤

ò

ઠે

ઠે

à

```
Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 AA; 17180 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSOKA8 CANFA PRELIMINARY;
QSOKA8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=nm23-C2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ransferase.
                                                                  Name=NME1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NM23-C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEPTARE
   SOUTH THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FAGLVKYMHSGPVVAMVWEGLMVVKTGRVMLGETNPADSKPGTIHGDFCIQVGRNIHGS 120
   76 TGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSD 135
                                       61 AGLVKYWHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yu J., Meng Y., Wang Z., Hansen C., Li C., Moore S., "Analysis of sequences obtained from constructed full-length bovine CDNA libraries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bos.
NCBI_TaxID=9913,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO, GO:0005224; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005521; F:ATP binding; IEA.
GO; GO:0004550; F:Ather each diphosphate kinase activity; IEA.
GO; GO:0004550; F:transferase activity; IEA.
GO; GO:0016741; P:CTP biosynthesis; IEA.
GO; GO:0006183; P:CTP biosynthesis; IEA.
GO; GO:000628; P:CTP biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 85.4%; Score 740; DB 2; Length 152; Best Local Similarity 92.1%; Pred. No. 3.3e-62; Matches 140; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AY911378; AAW82141.1; -; mRNA. SWR; Q56JV4; 5-152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 AA; 17260 MW; D1DB47DFC731B056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSVKSAEKEISLWFOPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 48, Created)
(Rel. 48, Last sequence update)
(Rel. 48, Last annotation update)
                                                                                                                             SVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                  SVESAEKEIALWFRPEELVNYKSCAQNWIYE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00469; NDP_KINASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01243; NUCDPKINASE. SMART; SMO0562; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR012005; NDK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1
                                                                                                                                                                                                                                                                                                                                                 Q56JV4_BOVIN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001564; NDK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDP kinase NBR-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rissum=Lymphoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OSOKA9;
13-SEP-2005
13-SEP-2005
13-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDKA CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                136
                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
NDKA CANFA
                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                           DONE NO DE REPORTE DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DEL PROPERTICA DE LA PROPERTICA DEL PROPERTICA DE LA PROPERTICA DEL PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DEL PROPERTICA DEL PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DE LA PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTICA DEL PROPERTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44444
                                                           g
                                                                                                                                ð
                                                                                                                                                                                         유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
```

```
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FAGLVKYMQSGPVVAMVWEGLAVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MANSERTFIAIKPDGVORSLVGEIIKRFEGKGFRLIAMKLIQASEDLLKEHYIDLKDRPF 60
                                                                                                                                                                    NUCLEOTIDE SEQUENCE [MRNA].
Takahashi M., Une R., Fukushima K., Fujiki M., Misumi K., Miyoshi N.,
Endo Y., Oishi A., Akuzawa M.;
"Molecular cloning of canine nm23 cDNAs and their expression in normal
                                                                                                                                                                                                                                                                           15 MANSERIFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Canis familiaris (Dog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pros-phosphohistidine intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00469; NDP_KINASES; 1.
ATP-binding; Kinase; Magnesium; Metal-binding; Nuclear protein;
Nucleotide metabolism; Nucleotide-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 92.1%; Pred. No. 6.3e-62;
Matches 140; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
669D444D69380FE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 DSVESAEKEIGLWFQPEELVDYKSCAQNWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB207044; BAD97837.1; -; mRNA.
InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
Ffam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PR01243; NUCPKINASE.
ProDom; PD001018; NDK; 1.
SMART; SM00562; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
```

Gaps

н ;

```
Pongo pygmaeus (Orangutan).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Heart;
The German cDNA Consortium;
Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MASSERTFIAIKPDGVQRGLVGDIIKRFEQKGFRLVALKLIQASEDLLKEHYVDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sukri, Ozfran; 2-125.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0004540; F:mucleoside-diphosphate kinase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:000621; P:GTP biosynthesis; IEA.

GO; GO:0006228; P:GTP biosynthesis; IEA.

InterPro; IPR001564; NDK.

InterPro; IPR0012005; NNK-2.

Pfam; PF00334; NDK; 1.

PIRSF; PIRSF000735; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.6%; Score 732.5; DB 2; Length 153; 90.8%; Pred. No. 9.5e-61; ive 9; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 83.6%; Score 732; DB 2; Length 152; Best Local Similarity 90.1%; Pred. No. 1e-60; Matches 137; Conservative 10; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR857184; CAH89484.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                        9E1FB7F2C4C1C844 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17300 MW; 8D2D9361C94DC938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein DKFZp468E0516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 -DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GDSVESAEKEIALWFQPEELVDYRSCAQDWIYE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 AA
GO; GO:0006183; P:GTP biosynthesis; IEA.
GO; GO:0006228; P:UTP biosynthesis; IEA.
InterPro; IPR001564; NDK.
InterPro; IPR012005; NDK-2.
Pfam; PF00334; NDK; 1.
PIRSF; PIRSF000735; NDK; 1.
PRINTS; PRO1243; NUCDPKINASE.
PRODOM; PD001018; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00562; NDK; 1.
PROSITE; PS00469; NDP_KINASES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        153 AA; 17198 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR01243; NUCDPKINASE
ProDom; PD001018; NDK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pongo pygmaeus (Orangutan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSRFH3_PONPY PRELIMINARY;
QSRFH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 90.8
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l protein.
152 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00562; NDK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=DKFZp468E0516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q5RFH3; 2-152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
SEQUENCE 15
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PONPY
                                                                                                                                                                                                                                                                                                                                                                        Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOW KERN COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF THE COOCCOS OF T
            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
Takahashi M., Une R., Fukushima K., Fujiki M., Misumi K., Miyoshi N., Endo Y., Oishi A., Akuzawa M.;
"Molecular cloning of canine nm23 cDNAs and their expression in normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAHQERTFIAIKPDGVQRGLVGDIVKRFEQKGFRLVAMKFLRASEDLLKEHYIDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
    Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name-NDPK-A;
Cavia porcellus (Guinea pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMR; Q99NI2; 5-153.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0004550; F:nucleoside-diphosphate kinase activity; IEA.
GO; GO:0006241; P:CTP biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                        | Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases. |
| Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases. |
| R EMBL, AB207045; BAD97838.1; -; MRNA. |
| R EMR, Q50KA8; 2-152. |
| InterPro; IPR012064; NDK. |
| InterPro; IPR012005; NDK. 1. |
| P FRSF; PIRSP000735; NDK; 1. |
| P FRNTS; PR01243; NUCDPKINASE. |
| R ProDom; PD001018; NDK; 1. |
| R PROSTITE; PS00469; NDP, KINASES; NDP, KINASES; NDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 83.9%; Score 735; DB 2; Length 15 Best Local Similarity 90.1%; Pred. No. 5.5e-61; Matches 137; Conservative 10; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
TISSUB=Cardiac endothelium;
Buxton I.L.O., Kaiser R.A., Oxhorn B.C., Cheek D.J.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- SINILARITY: Belongs to the NDK family.
EMBL; AYON705; AAK00527.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buxton I.L.O.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nucleoside diphosphate kinase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 DSVKSAEKEISLWFKPEELVDYKSCAFDWIYE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Cardiac endothelium;
Buxton I.L.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q99NI2 CAVPO PRELIMINARY;
Q99NI2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10141;
                                                                                                                                                       NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
```

셤

ઠે

셤

ö

Gaps

```
8 6 6 6 6
```

134	120
75 FTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIHGS 134	61 FPGLVKYMNSGPVVAMVWEGLNVVKTGRLMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 120
75	61

Search completed: December 16, 2005, 16:37:01 Job time : 155.472 secs

This Page Blank (uspto)

```
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20, Appl
                                                                           ; Search time 34.4528 Seconds (without alignments)
398.346 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 933, Psequence 2, Apr
Sequence 3, Apr
Sequence 5, Apr
Sequence 5, Apr
                                                                                                                                                          1 QSQPAVKPCHLKGTMANSER......WFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4,
Sequence 4,
Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2
Sequence 3
Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                             Issued Patents AA:*

. /cgm2_6/ptodata/1/iaa/5_COMB.pep:*

. /cgm2_6/ptodata/1/iaa/6_COMB.pep:*

. /cgm2_6/ptodata/1/iaa/H_COMB.pep:*

. /cgm2_6/ptodata/1/iaa/H_COMB.pep:*

. /cgm2_6/ptodata/1/iaa/RECOMB.pep:*

. /cgm2_6/ptodata/1/iaa/RECOMB.pep:*

. /cgm2_6/ptodata/1/iaa/RecoMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-09-460-532-3
S-09-513-999C-5323
S-09-248-796A-18029
S-09-183-861-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-335-948-5
US-07-806-932B-1
US-09-173-825-4
US-09-135-948-4
US-09-335-948-4
US-09-460-532-4
US-09-335-948-2
US-09-335-948-2
US-09-335-948-2
US-09-335-948-2
US-09-335-948-1
US-09-335-948-2
US-09-335-948-1
US-09-335-948-1
US-09-335-948-1
US-09-345-55
US-09-348-1
US-09-460-532-3
US-09-548-199-842-3
US-09-199-842-3
US-09-199-842-5
US-09-199-842-5
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
US-09-199-842-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-09-022-765-20
3-09-551-974A-20
3-09-565-501A-20
3-09-639-206A-20
3-09-874-923-20
                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-798-841-20
                                                                                                                                                                                                                             572060 seqs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            December 16, 2005, 16:31:59
                                                     protein search, using sw model
                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match Length DB
                                                                                                                                 US-10-074-694-3
               Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                      OM protein -
                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
No.
```

ö

Gaps ; 0

Length 184;

Query Match
90.6%; Score 794; DB 2; Length 18
Best Local Similarity 91.5%; Pred. No. 2.4e-85;
Matches 150; Conservative 4; Mismatches 10; Indels

TYPE: PRT ORGANISM: Homo Sapiens

US-09-335-948-5

122 140

80 62

요

g à

Š

3 QPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL

RESULT 2
US-07-806-932B-1
Sequence 1, Application US/07806932B
Patent No. 6423836
GENERAL INFORMATION:

63 KEHYTDLKORPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF

		ì	,	:	•	•	000		000000	101
87	76.	n i	· ·	9 6	٧,	100-00	3 6 6		antianhae	1
29	481	4	٠.	187	٦.	-80-80	679		acuentes	
30	481	24	o.	187	N	ns-09-	-199-842-1		Sequence	1, Appli
31	481	54	6.	187	7	-60-SD	US-09-460-532-1		Sequence	
32	481	54	6.	187	~	US-09-	US-09-538-092-823		Sequence	
33	472	23	6.	158		US-09-	US-09-443-184-59		Sequence	59, Appl
3.4	466	23	Ŋ	231		US-10-	US-10-227-035-4		Sequence	
35	433	49	4.	159		-60-SD	US-09-134-001C-32	216	Sequence	3216
36	394	45	٥.	161		-60-SD	US-09-358-972-91		Sequence	91,
3.7	394	45	٥.	161		-60-SD	US-09-790-417-91		Sequence	91, Ag
38	348	39	.7	137	7	-60-SD	US-09-583-110-363	6	Sequence	3639,
39	348	σ	٠.	148		-60-sn	US-09-107-433-364	co Co	Seguence	3645,
40	328	~		154		US-09-107	.107-532A-600(	00	Seguence	6000,
41	320	36	ī.	145		US-09-937	.937-296-1		Sequence	1, App
4.2	320	36		145		US-09-902	-540-103	81	Sequence	2
. 4. . 6.	318	36	<u>ر</u> ا	145		US-09-937	-296-2		Sequence	2, A
	308.5		N	200		-60-SD	-252-991A-2298	989	Seguence	22
	m	35	0	153		•	θ.	0	Sequence	7960, Ap
RESULT 1 118-09-335-948-5	- 948-	,,								
Sequence	5,2	tpp11	catio	5, Application US/09335948	/0933	5948				
; Patent No. 6329198	No. '6	32919	8							
; GENERAL	INFO	MATI	••							
; APPLICANT: National	ANT:	Natio		Institutes	cutee	ö	Health			
; APPLICANT:	NT:	Charles		'n	ភ្ជ					
; APPLICANT:	ANT:	Patr	Patricia	S	. Steeg					
, APPLICANT:	ANT:	Lance A.	e A	Liotta	r a					
	OF INVENTION:	ENT	 8	PRODUC	Ó	AND	PRODUCTION AND USE OF HUMAN NM23	NMZ3	PROFEIN	
, TITLE C	OF IN	INVENTION:	5 5 5	AND .	HILL I	AND ANTIBODIES	THEKEFOR			
; Filb KBFBKBNCB: 14014.0321	SFBRE	9	7.00	200.1	1	(6/00/				
; CURRENT	r APPI	L P		NOMBE	ž ;	APPLICATION NUMBER: US/US/335	7,			
CORRENT	7	5 T	AIE	FILING DATE: 1999-06-18						
	APPLI(	ATIO	N N	APPLICATION NUMBER: 08/475	08/4	175,634				
	FILIN	3 DAT	ન ¦ કાં	FILING DATE: 1995-06-07	70-9	-				
	APPLI(	ATIO	N N	APPLICATION NUMBER: 07/806	07/6	, 93	7		•	
	PILIN	3 DAT	H .	FILING DATE: 1991-12-11	1	0				
, PRIOR ,	APPLI(	ATIO		APPLICATION NUMBER: 0//	\ \ \ \ \	422,801				
<b>D</b>		OF SECTIONS.	1 00	4	1					
SOFTWARE	E: F:	FastSEO	o for		dows	Windows Version 4.	on 4.0			
SEO ID NO	ഗ		ı							
LENGTH		₹#								
יייייייייייייייייייייייייייייייייייייי	ρ									



```
135 DSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                  COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,825
FILING DATE: FILED Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                          APPLICALL...
PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 468542
                             STREET: 31/7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-713-825-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-199-842-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 KEHYTDLKDRPFFTGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 OPAVKPCHLKGTMANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 OPOFKPKOLEGTMANCERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFWQASEDLL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 90.6%; Score 794; DB 2; Length 184; Best Local Similarity 91.5%; Pred. No. 2.4e-85; Matches 150; Conservative 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 CIQVGRNIIHGSDSVKSAEKEISLWFQPEELVEYKSCAQNWIYE 166
KING, ET AL.
FENTION: PRODUCTION AND USE OF HUMAN
ESPITION: HUMAN NM23 PROTEIN AND ANTIBODIES
FENTION: THEREPOR
               TITLE OF INVENTION: PRODUCTION AND USE OF HUMAN TITLE OF INVENTION: HUMAN NM23 PROTEIN AND ANTIETITLE OF INVENTION: THEREPOR TITLE OF INVENTION: THEREPOR NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESSE: CRECHI & STEWART STREET: 6 BECKELA, BRINE, BAIN, GILFILLIAN, ADDRESSEE: CRECHI & STEWART STREET: 6 BECKER PARM ROAD STATE: NEW JERSEY COUNTRY: USA ZIP: 07068
COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER: 18A PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE: HUMAN NM 23-H28
PUBLICATION INFORMATION:
PUBLICATION INFORMATION: 1: FROM -32 TO 152
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/806,932B
FILING DATE: 11 december 1991
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,801
FILING DATE: 18 october 1989
ATTORNEY/AGENT INFORMATION:
NAME: CAPELLO, SUSAN A.
REGISTRATION NUMBER: 34,560
REFERENCE/DOCKET NUMBER: 469200-TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 184 AMINO ACID RESIDUES
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                        PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
SOFTWARE: DW4.V2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-806-932B-1
```

```
75 FTGLVKYMHSGPVVAMVWEGLAVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGS 134
                                                                                                                                                                                                     61 FAGLVKYMHSGPVVAMVWEGLAVVKTGRVWLGETNPADSKPGTIRGDFCIQVGRNIHGS 120
                                                                                                           15 MANSERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVGLKFLQASEDLLKEHYTDLKDRPF
                                                         Gaps
Query Match

86.6%; Score 759; DB 1; Length 152;
Best Local Similarity 94.1%; Pred. No. 2.4e-81;
Matches 143; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09199842
Patent No. 6087125
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
STREET: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
~wwpITFER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.
ZIP: 94304
```

Sequence 4, Application US/08713825
Patent No. 5874285
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN NM23-LIKE PROTEIN
UNMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:

RESULT 3 US-08-713-825-4

g ઠે

ઠે

		· •
		Ĺ